

GenCore version 5.1.3
(c) 1993 - 2003 Compu

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st 100 summaries

EST:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	7.78	30.3	877	9	AL5A1041	AL5A1041 AL5A1041
2	6.58	27.2	1002	14	B0052308	B0052308 AGENCOURT
3	6.31	24.6	794	12	B6677567	B6677567 6026224118
4	6.29	24.5	966	14	B0054265	B0054265 AGENCOURT
5	6.19	24.1	1020	14	B0054281	B0054281 AGENCOURT
6	6.05	23.6	1069	14	B0052468	B0052468 AGENCOURT

[illegible]

80 61 2.4 982 17 AF011221
81 61 2.4 1080 14 BM810567
82 61 2.4 1189 12 BG611991
83 60 2.3 490 17 BHL52886
84 59 2.3 226 12 BP854329
85 59 2.3 263 9 AB825185
86 59 2.3 312 17 AF166285
87 59 2.3 317 9 AA573000
88 59 2.3 349 10 AW770050
89 59 2.3 379 17 A0580711
90 59 2.3 382 9 AA219031
91 59 2.3 383 12 BF7515195
92 59 2.3 409 13 BG952898
93 59 2.3 420 9 AA835931
94 59 2.3 422 9 AA743968
95 59 2.3 440 17 B17487
96 59 2.3 447 17 A0038575
97 59 2.3 518 17 A0412294
98 59 2.3 524 12 BF737749
99 59 2.3 540 9 AL699257
100 59 2.3 592 14 BQ272418

ALIGNMENTS

RESULT 1
AL541041 877 bp mRNA linear EST 16-FEB-2001
DEFINITION AL541041 LTI FL002_P11 Homo sapiens cDNA clone CS0DE005YK23 5 prime
LOCUS AL541041
ACCESSION AL541041
VERSION AL541041.1 GI:12871733
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 877)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1..877
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DE005YK23"
/clone_1id="LTI_FL002_P11"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by life
technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
liang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 192 a 262 c 251 g 170 t 2 others
ORIGIN

Query Match 30.3% Score 778; DB 9; Length 877;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 828; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 29 CAAAGACCCACCGCTGTCTCTGTGACAGAGCTCAAAGAGCCCTGGGCTTCCTCC 88
Db 1 CAAAGACCCACCGCTGTCTCTGTGACAGAGCTCAAAGAGCCCTGGGCTTCCTCC 60

Qy 89 TGGCTGGCTGTGTGGAGAGGTTCCCAAGTCAGAACTCCCTAAGAGCATGGGAGC 148
Db 61 TGGCTGGCTGTGTGGAGAGGTTCCCAAGTCAGAACTCCCTAAGAGCATGGGAGC 120
Qy 149 TGATTCATCTCTGTGTGTAACAATCTGTGATCTGAGACAGATCTGTGATCTCCAAACCA 208
Db 121 TGATTCATCTCTGTGTGTAACAATCTGTGATCTGAGACAGATCTGTGATCTCCAAACCA 180
Qy 209 CACCTACCTCTCTCTGAGATCTCTCCAGAGCTGAGAGATCTGGGTCTCTAGACCA 268
Db 181 CACCTACCTCTCTCTGAGATCTCTCCAGAGCTGAGAGATCTGGGTCTCTAGACCA 240
Qy 269 AGGACATGGACATTTTCCAGAGAGGCCCCCAAGCCCTTAACCTGTCCGACAGAGATG 328
Db 241 AGGACATGGACATTTTCCAGAGAGGCCCCCAAGCCCTTAACCTGTCCGACAGAGATG 300
Qy 329 CGTCTCAGAGAGCTGTCTTCCCAAGCTTTGATGACAAACCAATTTCTCTGATGATGT 388
Db 301 CGTCTCAGAGAGCTGTCTTCCCAAGCTTTGATGACAAACCAATTTCTCTGATGATGT 360
Qy 389 GCTTCTGAGCTCTGTCTGAGAGAAAGATGAGAGCTGAGAGAGAGAGAGAGAGAGAGAG 448
Db 361 GCTTCTGAGCTCTGTCTGAGAGAAAGATGAGAGCTGAGAGAGAGAGAGAGAGAGAGAG 420
Qy 449 CAAAGCCAGCTTGAATTCCTGTCTCAAGGACAGGACCTGTGACATGAGAGAGAGA 508
Db 421 CAAAGCCAGCTTGAATTCCTGTCTCAAGGACAGGACCTGTGACATGAGAGAGAGA 480
Qy 509 GAAACCAAGGACAGAGCTGTCTTCCAGAGATTTCCGAGAGAGAGAGAGAGAGAGAGAG 568
Db 481 GAAACCAAGGACAGAGCTGTCTTCCAGAGATTTCCGAGAGAGAGAGAGAGAGAGAGAG 540
Qy 569 CGCTGACATCTGGGAGGACATTTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 628
Db 541 CGCTGACATCTGGGAGGACATTTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Qy 629 TGTCTGAGCTCTGAGAGAGATTTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 688
Db 601 TGTCTGAGCTCTGAGAGAGATTTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Qy 689 ATGGTGTCTGTATAGAGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 748
Db 661 ATGGTGTCTGTATAGAGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Qy 749 GGAACCTGAGAGAGGCTTCTCTATCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 808
Db 721 GGAACCTGAGAGAGGCTTCTCTATCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Qy 809 TGTCTGCTGCTCTGAGGCTTCTCTATCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 857
Db 781 TGTCTGCTGCTCTGAGGCTTCTCTATCTCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 829

RESULT 2
LOCUS B0052308 1002 bp mRNA linear EST 28-MAR-2002
DEFINITION B0052308 NIH-MGC_106 Homo sapiens cDNA clone IMAGE:593542
ACCESSION B0052308
VERSION B0052308.1 GI:19811648
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1002)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: csa@bbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, D8S/NCI

CNDA Library Preparation: Rubin Laboratory
 CNDA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>

Plate: LNCM218 row: d column: 23
 High quality sequence stop: 670.
 Location/Qualifiers

FEATURES

source

1.1002
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5933542"
 /clone_id="NIH_MGC_106"
 /issue_type="natural killer cells, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; CNDA made by oligo-dt priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-CNDA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."
 BASE COUNT 221 a 296 c 288 g 197 t
 ORIGIN

Query Match 27.2%; Score 698; DB 14; Length 1002;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 748; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

350 CCAAGCCTTGTATGACAAACAAATTCCTGATGATGCTTGAATGCTCTGCGAG 409
 31 CCAAGCCTTGTATGACAAACAAATTCCTGATGATGCTTGAATGCTCTGCGAG 90
 410 GAAACAATGGAAGTCTGCCAGAGAGAAATCTTGCACCAAGCCCAAGTTGCT 469
 91 GAAACAATGGAAGTCTGCCAGAGAGAAATCTTGCACCAAGCCCAAGTTGCT 150
 470 CTGTCACAGGCGAGGACCTGTGACCATGAGAGAGAGAGAGAGAGAGAGAGAG 529
 151 CTGTCACAGGCGAGGACCTGTGACCATGAGAGAGAGAGAGAGAGAGAGAGAG 210
 530 CCTGAGGCAAGTTTCCCGGAGGTGCGCCGCGAGGCTGTGAGACTCGAGGAGCAT 589
 211 CCTGAGGCAAGTTTCCCGGAGGTGCGCCGCGAGGCTGTGAGACTCGAGGAGCAT 270
 590 TGACCATGCTCTGAGAGATGAGACTGTGAGAGAGAGAGAGAGAGAGAGAGAG 649
 271 TGACCATGCTCTGAGAGATGAGACTGTGAGAGAGAGAGAGAGAGAGAGAGAG 330
 650 AGTATACATCCCAAGGCTCACGTGCGCAAGTCTCCATGAGGTGATGAGAGCC 709
 331 AGTATACATCCCAAGGCTCACGTGCGCAAGTCTCCATGAGGTGATGAGAGCC 390
 710 TGAGCAGGAG 769
 391 TGAGCAGGAG 450
 770 TCATCCGAG 829
 451 TCATCCGAG 510
 830 CTGACATCTGGAGACCGGATCAGACATCAGAGATCCAGCTGAGCAATGAGCTGT 889
 511 CTGACATCTGGAGACCGGATCAGACATCAGAGATCCAGCTGAGCAATGAGCTGT 570
 890 ACATCTCAACCGGCTTCACTTCCCTCACTCAGGCGCTGTGAGCAATGAGCTGT 949
 571 ACATCTCAACCGGCTTCACTTCCCTCACTCAGGCGCTGTGAGCAATGAGCTGT 630
 950 TGAGCAGGAG 1009

Db 631 TGCGGATGACATCTGCTGCTCAAGAGCCCTGTGCTCTGAGAGGCTGCGCC 690
 1010 TCCCTGGAGAGATATATACCTTACTGATGCTGTGAGAGAGAGAGAGAGAGAG 1069
 691 TCCCTGGAGAGATATATACCTTACTGATGCTGTGAGAGAGAGAGAGAGAGAG 750
 1070 AGCTGGAG 1098
 751 AGCTGGAG 779

RESULT 3

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CNDA Library Preparation: Life Technologies, Inc.
 CNDA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LNCM1061 row: d column: 05
 High quality sequence stop: 790.
 Location/Qualifiers

FEATURES

source

1.794
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4748884"
 /clone_id="NCI_CGAP_Skn4"
 /issue_type="squamous cell carcinoma"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. primer: oligo dT.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 192 a 229 c 212 g 161 t
 ORIGIN

Query Match 24.6%; Score 631; DB 12; Length 794;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

946 GAGCTGCGAGATGACATCTGCTGCTCAAGAGAGAGAGAGAGAGAGAGAGAG 1005
 17 GAGCTGCGAGATGACATCTGCTGCTCAAGAGAGAGAGAGAGAGAGAGAGAG 76
 1006 CCGCTCCCTGGCAAGATATACCTTACTGATGCTGTGAGAGAGAGAGAGAGAG 1065
 77 CCGCTCCCTGGCAAGATATACCTTACTGATGCTGTGAGAGAGAGAGAGAGAG 136
 1066 AAGAGCTGAGACAGCTCTCTGTTTTCAGAGCTGCCAGAGAGAGAGAGAGAG 1125
 137 AAGAGCTGAGACAGCTCTCTGTTTTCAGAGCTGCCAGAGAGAGAGAGAGAG 196
 1126 AGTGAAGGCTCTCCGAGAGAGCTCTGAGCTTCAATGAGCTGAATGAGAGAG 1185
 197 AGTGAAGGCTCTCCGAGAGAGCTCTGAGCTTCAATGAGCTGAATGAGAGAG 256

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLM at:

http://image.llnl.gov

plate: L10M215 row: 3 column: 11

High quality sequence stop: 556.

FEATURES

Location/Qualifiers

1..1020

Source

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5936362"

/clone_lib="NIH_MGC_106"

/tissue_type="natural killer cells, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 219 a 311 c 263 g 204 t 3 others

ORIGIN

Query Match 24.1%; Score 619; DB 14; Length 1020;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 719; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 208 ACACTAGCCTCTCCCTGAAATCTCCAGGCTGAGAGATTCTGGTGTCTAGAGACC 267

Db 5 AACCTAGCCTCTCCCTGAAATCTCCAGGCTGAGAGATTCTGGTGTCTAGAGACC 64

Oy 268 AAGGACCTGGCAGACTTCCAGAGAGGCGCCCAAGCCCTAACTGTCAGCCAGAGCAT 327

Db 65 AAGGACCTGGCAGACTTCCAGAGAGGCGCCCAAGCCCTAACTGTCAGCCAGAGCAT 124

Oy 328 GGGTCTCAGCAGAGCTGTCTCCCAAGCCTTTGATGCAAACTATTTCCCTGATGATG 387

Db 125 GGGTCTCAGCAGAGCTGTCTCCCAAGCCTTTGATGCAAACTATTTCCCTGATGATG 184

Oy 388 TGGCTCTGAGTGTCTCTGAGAGAACATGGAAGTCTGCGCAGAGAGAAATCTG 447

Db 185 TGGCTCTGAGTGTCTCTGAGAGAACATGGAAGTCTGCGCAGAGAGAAATCTG 244

Oy 448 CCAAGCCCAAGCTTGAAGTCTCTGTCAGAGGCAAGGACCTGTGACCATGAGAGAG 507

Db 245 CCAAGCCCAAGCTTGAAGTCTCTGTCAGAGGCAAGGACCTGTGACCATGAGAGAG 304

Oy 508 AAGAGCAAGGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 567

Db 305 AAGAGCAAGGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 364

Oy 568 TGGCTGAGACTGGGGAGCCATTGACATGCTCTGAGAGATGAGACTGGTGGAGCGTG 627

Db 365 TGGCTGAGACTGGGGAGCCATTGACATGCTCTGAGAGATGAGACTGGTGGAGCGTG 424

Oy 628 CTGTCTGAGAGCTCAGGCAAGAGATATTAACATCCCGAGGCTCAAGTGGCCAAAGCTCC 687

Db 425 CTGTCTGAGAGCTCAGGCAAGAGATATTAACATCCCGAGGCTCAAGTGGCCAAAGCTCC 484

Oy 688 CATGGTGGCTGTATGAGGCTCTGAGCAGGAGAAAGAGAGAACTGTGTGTTACTT 747

Db 485 CATGGTGGCTGTATGAGGCTCTGAGCAGGAGAAAGAGAGAACTGTGTGTTACTT 544

Oy 748 GGGAGACCTGGAGGGGCTTCTCATCCGGAGAGCCAGACAGAGAGAGCTCTTCTCT 807

Db 545 GGGAGACCTGGAGGGGCTTCTCATCCGGAGAGCCAGACAGAGAGAGCTCTTCTCT 604

Oy 808 CTGTCAATCCGCTCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 867

Db 605 CTGTCAATCCGCTCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 664

Oy 868 TGCCTTGA CAATGGCTGGCTTGA CTCA CGCGGCTCA CTTCCCTCACTCAGGCG 927

Db 665 TGGCTTGA CAATGGCTGGCTTGA CTCA CGCGGCTCA CTTCCCTCACTCAGGCG 724

Oy 928 C 928

Db 725 C 725

RESULT 6

LOCUS

LOCUS

DEFINITION

AGNCOURT 686422 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5933772

5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

human.

human.

human.

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Qy	567	GTGCTGAGACTGGGGAGGCCATTGACCATCTGCTCTGAGAGATGGAGCTGGTGAACGGT	626
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Qy	627	GCTGTCGAGACTTCGAGAGAGAGATATACATCCCAAGCTCCACCTGGGCTAAAGTCTC	686
Db	301	GCTGTCGAGACTTCGAGAGAGAGATATACATCCCAAGCTCCACCTGGGCTAAAGTCTC	360
Qy	687	CCATGGGTGCTGTATGAGGGGCTTGAGAGAGAGAGAAAGCAGAGATCTGTTGTATCC	746
Db	361	CCATGGGTGCTGTATGAGGGGCTTGAGAGAGAGAGAAAGCAGAGATCTGTTGTATCC	420
Qy	747	TGGGAACTCGTGAAGGGGCTTCTCATCTCGGGAGAGACAGAGAGAGAGCTCTTATCTC	806
Db	421	TGGGAACTCGTGAAGGGGCTTCTCATCTCGGGAGAGAGAGAGAGAGAGCTCTTATCTC	480
Qy	807	TCTGTCACTCCGCTTCAGCGGCGCTTCGATCTGGGACCGGATCAGACATCAACGATCTCA	866
Db	481	TCTGTCACTCCGCTTCAGCGGCGCTTCGATCTGGGACCGGATCAGACATCAACGATCTCA	540
Qy	867	CTGCCTTGACAAATGGCTGGCTGTACATCTCACCGGCGCTTACCTTCCCTCATCTCCAGGC	926
Db	541	CTGCCTTGACAAATGGCTGGCTGTACATCTCACCGGCGCTTACCTTCCCTCATCTCCAGGC	600
Qy	927	CCTGG 931	
Db	601	CCTGG 605	

RESULT 7	
AL568702/c	
LOCUS	854 bp mRNA linear EST 16-FEB-2001
DEFINITION	AL568702 L11_F1002.pl1 Homo sapiens cDNA clone CSDBE005TK23 3 prime
ACCESSION	AL568702
VERSION	AL568702
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eumetazoa; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	Li, W. B., Gruber, C., Udesse, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	Contact: Genoscope

FEATURES
Genoscope - Centre National de Séquençage
BP 191 91006 EVRY cedex - France
Email: seq@genoscope.cns.fr, Web : www.genoscope.cns.fr
Location/Qualifiers

```

source
1. .854
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cclone="CSODP005YK23"
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/lab_host="DH10B"
/notes="Organ: Placenta; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com"

```

Query Match 23.4%; Score 600; DB 9; Length 854;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 600; Conservative 0; Mismatches 0; Gaps 0.

Oy	1841	TTTTTTTGAAGAGAGATCTTGCCCTGTGGCCCAATGCTGAGTGAAGTGAAGAGATCTCAG	1900
Db	602	TTTTTTTGAAGAGAGATCTTGCCCTGTGGCCCAATGCTGAGTGAAGTGAAGAGATCTCAG	543
Oy	1901	CTCACTGCAACCTCCATCTCTGAGATTAAACAATTCTCTGCTCCAGCTCCGAATTAG	1960
Db	542	CTCACTGCAACCTCCATCTCTGAGATTAAACAATTCTCTGCTCCAGCTCCGAATTAG	483
Oy	1961	CTGGGATTACAGGCGTAAACCAACCAATGCTGGCTAAATTTTTTTTATTTTATTTAGTACAT	2020
Db	482	CTGGGATTACAGGCGTAAACCAACCAATGCTGGCTAAATTTTTTTTATTTTATTTAGTACAT	423
Oy	2021	GGGGTTTCAACAATGGGCCAGGCTGAGTGCAGAACTCCAGACCTCAGTGAATCCACCCAC	2080
Db	422	GGGGTTTCAACAATGGGCCAGGCTGAGTGCAGAACTCCAGACCTCAGTGAATCCACCCAC	363
Oy	2081	CTTGGCCTCCCAAACTGTGGGATTACAGGTGTAGCCACGCAACCAGCTTAGCTCTCA	2140
Db	362	CTTGGCCTCCCAAACTGTGGGATTACAGGTGTAGCCACGCAACCAGCTTAGCTCTCA	303
Oy	2141	GATCTCTATTATTTTGTGGCTTAACAATTCCTCAGCAACAGGCGCTTGCATCTTTGG	2200
Db	302	GATCTCTATTATTTTGTGGCTTAACAATTCCTCAGCAACAGGCGCTTGCATCTTTGG	243
Oy	2201	CCGAATTAAAAAATAACAACCTCTTAAGCTTAGCACTGTGAGTGGCCAGGACCTCAGT	2260
Db	242	CCGAATTAAAAAATAACAACCTCTTAAGCTTAGCACTGTGAGTGGCCAGGACCTCAGT	183
Oy	2261	GCTGGGCAAGGGGATCAGAAAGTGTCTAAGCCTCTCTCCAAATGCCAGAGGAGCA	2320
Db	182	GCTGGGCAAGGGGATCAGAAAGTGTCTAAGCCTCTCTCCAAATGCCAGAGGAGCA	123
Oy	2321	CAGCCTACACAATAATCCAGCCTTGAATTTTCCCTGCTCTCCATTAACAGAAAGGTCT	2380
Db	122	CAGCCTACACAATAATCCAGCCTTGAATTTTCCCTGCTCTCCATTAACAGAAAGGTCT	63
Oy	2381	GCTGGATCCGCTTAAGGATCAAGGAGAGAGAAAGAAAGGATGGGGTGGGAGGACCCCC	2440
Db	62	GCTGGATCCGCTTAAGGATCAAGGAGAGAGAAAGAAAGGATGGGGTGGGAGGACCCCC	3

RESULT	8
LOCUS	AL844325
DEFINITION	Al844325 677 bp mRNA
ACCESSION	AL844325 pool_YR_1ib_v_SPD Homo sapiens cDNA, mRNA sequence.
VERSION	AL844325.1 GI:22019105
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Ekwall-Ota; Weibacota; Urobacota; Canatada; Vercubacota; Euterebota; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 677)
Asricoft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckie, E.J. and Sheridan, E.
Homo sapiens EST sequence
Unpublished (2002)
Contact: The Sanger Centre
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquerry@sanger.ac.uk
Sanger Centre name : scdd10827.400489S
Homo sapiens EST sequence. This sequence was generated as part of The Wellcome Trust Sanger Institute program to identify and annotate genes in the human genome. Incomplete or unconfirmed genes are experimentally analysed using a variety of cDNA library resources. This sequence was obtained from a PCR product generated from a pool of up to 100,000 cDNA clones derived from
http://www.sanger.ac.uk/Teams/Team69/.
Location/Qualifiers
L. 677

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20"
/clone_1b="pool_YT_11b_v_SPD"
/notes="Organ: breast; Vector: pZERO-1; Site_1: SpH1;
Site_2: SpH1; Ductal carcinoma in situ, high-grade, comedo
of 41 yo female. Library constructed in the laboratory
of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."
```

Query Match	21.7%	Score 557;	DB 9;	Length 677;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 677; Conservative	0;	Mismatches	0;	Indels 1; Gaps 1;

Oy	1680	TGCGCTTAAGGGGAAAGAAAGCTGACATGATGTTTACCGTAGCAGAGATCTTGATG	1733
Db	1	TGGCTTAAGAGGAAAGGAAAGCTGATATGATGTTTACCGTAGCAGAGATCTTGATG	60
Oy	1740	GTCCAGGCTCTATGTGATCCTCGAGCCAAAGAAAGAATTCCGACAGTCTTAGGTCCTCA	1799
Db	61	GTCCAGGCTCTATGTGATCCTCGAGCCAAAGAAAGAATTCCGACAGTCTTAGGTCCTCA	120
Oy	1800	AATGACCCCAATTGAGACCAACAGCCCAAGCTCTTTTCTTTTCTTTTGTGACAGGATCT	1858
Db	121	AATGACCCCAATTGAGACCAACAGCCCAAGCTCTTTTCTTTTCTTTTGTGACAGGATCT	179
Oy	1860	TGCGCTGAGCCCACTCGAGAGTGCATATGGCACAGATCTGAGCTACATGCACTTCCATCT	1919
Db	180	TGCGCTGAGCCCACTCGAGAGTGCATATGGCACAGATCTGAGCTACATGCACTTCCATCT	239
Oy	1920	CCTGGAATCAAAACAATCTCTGCTCAGCTTCAGAAATGCTGGGATTAACAGCCGTACA	1979
Db	240	CCTGGAATCAAAACAATCTCTGCTCAGCTTCAGAAATGCTGGGATTAACAGCCGTACA	299
Oy	1980	CCACCAATCCCTGAGCTAATTTTTTGTATTTTGTATTTTGTATTTTGTATTTTGTATTTTGT	2039
Db	300	CCACCAATCCCTGAGCTAATTTTTTGTATTTTGTATTTTGTATTTTGTATTTTGTATTTTGT	359
Oy	2040	CAGGCTGTGATCCAACTCTGATCTCAGGATATCCACCACTTTGGCTCCCAAAAGTCT	2099
Db	360	CAGGCTGTGATCCAACTCTGATCTCAGGATATCCACCACTTTGGCTCCCAAAAGTCT	419
Oy	2100	GGGATTAACAGTGTGAGCCAGGACCAAGCCATGATCTCAGATCTCTATTTTCTATTTTGT	2159
Db	420	GGGATTAACAGTGTGAGCCAGGACCAAGCCATGATCTCTATTTTCTATTTTGTATTTGT	479
Oy	2160	GGCTTACCATTCCTCTAGACACTGAGCCCTGAGCCATCTGTGCGGATTAATAAATAACCC	2219
Db	480	GGCTTACCATTCCTCTAGACACTGAGCCCTGAGCCATCTGTGCGGATTAATAAATAACCC	539
Oy	2220	TCTTAAGTCTAGCACACTGCAAGTGAAGCCAGGACCTTAGTCTGGGACGGGAGATCAGA	2279
Db	540	TCTTAAGTCTAGCACACTGCAAGTGAAGCCAGGACCTTAGTCTGGGACGGGAGATCAGA	599
Oy	2280	AGGATCTAGGCTCTCTCCAAATGGCAAGAAGCAACAGGCTCTACCAATAATCCAG	2339
Db	600	AGGATCTAGGCTCTCTCTCCAAATGGCAAGAAGCAACAGGCTCTACCAATAATCCAG	659
Oy	2340	CCCTTGATTTCCCTGCTG 2357	
Db	660	CCCTTGATTTCCCTGCTG 677	

RESULT 9	AL844312/c	619 bp	mRNA	linear	EST 30-JUL-2002
LOCUS	AL844312				
DEFINITION	AL844312 pool_yt_1lb_v				
ACCESSION	AL844312				sapiens cDNA, mRNA sequence.
VERSION	AL844312.1				GI:22019094
KEYWORDS	EST.				
SOURCE	Hmanu.				
ORGANISM	Homo sapiens				

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
 Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo
 1 (bases 1 to 619)
 Ashcroft K., Bethel G., Bye J.M., Howell G.R., Huckle E.J. and
 Sheridan E.
 Homo sapiens EST sequence
 Unpublished (2002)
 Contact: The Sanger Centre

Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: hunguery@sanger.ac.uk
Sanger Centre name : sc0010818_400489A
Homo sapiens EST sequence. This sequence was generated as part of
the Wellcome Trust Sanger Institute program to identify and
annotate genes in the human genome. Incomplete or unconfirmed genes
are experimentally analysed using a variety of cDNA library
resources. This sequence was obtained from a PCR product generated
from a pool of up to 100,000 cDNA clones derived from
pool_YT11b_v_SBD cDNA library. Further information can be found at
<http://www.sanger.ac.uk/teams/team69/>.

FEATURES	Location/Qualifiers
source	1. 619
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/map="20"
	/clone_1b="pool YT 1b y SPD"
	/note="Organ: breast; Vector: pZPro-1; site 1: SpH1; site 2: SpH1; ductal carcinoma in situ, high-grade, comedo
	' from 41yo female. library constructed in the laboratory
	of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."
BASE COUNT	133 a 159 c 177 g 150 t
ORIGIN	

Query Match 20.2%; Score 519; DB 9; Length 619;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1085	TCGTGTTTCTGAAGTCGCAAGAGGAAGATCTTCTCATAGAGGTCCTCCGAGAT	1144
Db	570	TCCTGTTTCTGAAGTCGCCAGAGGAGAAAGTCTCTTCTCACTAAGGCTCCGGAGAT	511
Qy	1145	CCCTCAGCTTCTACATCAGGCTGAATGACGAGGCTGTCTCTTGGATGATGCTCAGGCC	1204
Db	510	CCCTCAGCTTCTACATCAGCTGTGAATGAAGAGGCTGTCTCTTGGATGATGCTCAGGCC	451
Qy	1205	AAAGGAGAAGCCAAAAGGAAAACCAAGGCTGCACACCTAGAACCCCAATTGAGCTCTTG	1264
Db	450	AAAGGAGAAGCCAAAAGGAAAACCAAGGCTGCACACCTAGAACCCCAATTGAGCTCTTG	391
Qy	1265	GGCACCACCAAGGCAAGGCTGTGCATCAGAGGAGGAGGGTGGGAACAAGAGTGCATCT	1324
Db	390	GGCACCACCAAGGCAAGGCTGTGCATCAGAGGAGGAGGGTGGGAACAAGAGTGCATCT	331
Qy	1325	AAGGTCCCACTGTGTACCTTGTCTTCTCTCTTAGGCTTTAGAGTCACTTCTCT	1384
Db	330	AAGGTCCCACTGTGTACCTTGTCTTCTCTCTTAGGCTTTAGAGTCACTTCTCTCT	271
Qy	1385	TCCAGTGCATGATCCACCTGCACCTCTAGTGCAGTGCAGAGAGGTGGACCAAGG	1444
Db	270	TCCAGTGCATGATCCACCTGCACCTCTAGTGCAGTGCAGAGAGGTGGACCAAGG	211
Qy	1445	CCAGGGTCCAAAAGAAATTAAGCCCTCGGAGGGATCTACCTAGTTAGTTCTTAGGTT	1504
Db	210	CCAGGGTCCAAAAGAAATTAAGCCCTCGGAGGGATCTACCTAGTTAGTTCTTAGGTT	151
Qy	1505	AGGGGTTTCCAGTACCATCTGATGCTCCGCTGTGATGAGGCCAATTCTACATCCCAACA	1564
Db	150	AGGGGTTTCCAGTACCATCTGATGAGCCCTGCTGTGATGAGGCCAATTCTACATCCCAACA	91
Qy	1565	TTTAAACAGGCCCCACCAACAAGGTAGAAACAACTCTTAGAGTCAACGAGAAATCATTTT	1624
Db	90	TTTAAACAGGCCCCACCAACAAGGTAGAAACAACTCTTAGAGTCAACGAGAAATCATTTT	31


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Oy 1625 CAGAAATCTACAGCTCTGTTGAGACAC 1654
Db 30 CAGAAATCTACAGCTCTGTTGAGACAC 1

RESULT 10
LOCUS AL844308 642 bp mRNA linear EST 30-JUL-2002
DEFINITION AL844308 pool_AK_11b_v_SPD Homo sapiens cDNA, mRNA sequence.
ACCESSION AL844308
VERSION AL844308.1 GI:22019090
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 642)
AUTHORS Ashcroft,K., Bethel,G., Bye,J.M., Howell,G.R., Huckle,E.J. and
Sheridan,E.
TITLE Homo sapiens EST sequence
JOURNAL Unpublished (2002)
COMMENT Contact: The Sanger Centre
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquerry@sanger.ac.uk
Sanger Centre name : scd10816.400489A
Homo sapiens EST sequence. This sequence was generated as part of
The Wellcome Trust Sanger Institute program to identify and
annotate genes in the human genome. Incomplete or unconfirmed genes
are experimentally analysed using a variety of cDNA library
resources. This sequence was obtained from a PCR product generated
from a pool of up to 100,000 cDNA clones derived from
pool_AK_11b_v_SPD cDNA library. Further information can be found at
http://www.sanger.ac.uk/Teams/Team69/.

FEATURES
source
1..642
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20"
/clone_11b="pool_AK_11b_v_SPD"
/note="Organ: Breast; Vector: pZERO-1; Site 1: SphI;
Site 2: SphI; Ductal carcinoma in situ, high-grade, comedo
, from 41 yo female. Library constructed in the laboratory
of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."
```

BASE COUNT 140 a 164 c 181 g 157 t

ORIGIN

```

Query Match 20.1%; Score 515; DB 9; Length 642;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1085 TCCTGTTTCTGAAGCTGCCACAGGGAGAGAGTCTTCTCAGTGAGGGTCTCCGGAGT 1144
Db 588 TCCTGTTTCTGAAGCTGCCACAGGGAGAGAGTCTTCTCAGTGAGGGTCTCCGGAGT 529

Oy 1145 CCTCAGCTCTACATCAGCGTGAATGAGAGGCTGCTCTTGGATGATGAGCTTGAAGCC 1204
Db 528 CCTCAGCTCTACATCAGCGTGAATGAGAGGCTGCTCTTGGATGATGAGCTTGAAGCC 469

Oy 1205 AAAGAGAGGCCAAAAGGAAAACCAAGGCTGCACACTTGAACCCCAATCAGCCTCTG 1264
Db 468 AAAGAGAGGCCAAAAGGAAAACCAAGGCTGCACACTTGAACCCCAATCAGCCTCTG 409

Oy 1265 GGACAGCCAGAGGCAAGGCTGTCACAGGGAGGAGGGGAGACAGAGGTGATCT 1324
Db 408 GGACAGCCAGAGGCAAGGCTGTCACAGGGAGGAGGGGAGACAGAGGTGATCT 349

Oy 1325 AGGGTCCACCTGACCTTGGCTCTTCTCTTAAAGCCCTTGAAGTCACTACTTCTT 1384
Db 348 AGGGTCCACCTGACCTTGGCTCTTCTCTTAAAGCCCTTGAAGTCACTACTTCTT 289

Oy 1385 TCCAGTGCATGATCCCACTGCGACCTCTAGTGAAGTGAAGAGAGGTGGACAGG 1444
Db 1385 TCCAGTGCATGATCCCACTGCGACCTCTAGTGAAGTGAAGAGAGGTGGACAGG 1444
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Db 288 TCCAGTGCATGATCCCACTGCGACCTCTAGTGAAGTGAAGAGAGGTGGACAGG 229
Oy 1445 CCAGGGTTCCAAAAAGAGAAATAGACCTCTCTGGGGGGTCTGACCTAGTATTGTTAGTT 1504
Db 228 CCAGGGTTCCAAAAAGAGAAATAGACCTCTCTGGGGGGTCTGACCTAGTATTGTTAGTT 169

Oy 1505 TGAGGTTTCAGTGCATCTGATGATGCGGCTGTTAGGCCCATTTACATCCCAACA 1564
Db 168 TGAGGTTTCAGTGCATCTGATGATGCGGCTGTTAGGCCCATTTACATCCCAACA 109

Oy 1565 TTAACGAGGCCCAACCCACAGAGGTGAAAACCAACC 1599
Db 108 TTAACGAGGCCCAACCCACAGAGGTGAAAACCAACC 74

RESULT 11
LOCUS AL844326 599 bp mRNA linear EST 30-JUL-2002
DEFINITION AL844326 pool_YT_11b_v_SPD Homo sapiens cDNA, mRNA sequence.
ACCESSION AL844326
VERSION AL844326.1 GI:22019106
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 599)
AUTHORS Ashcroft,K., Bethel,G., Bye,J.M., Howell,G.R., Huckle,E.J. and
Sheridan,E.
TITLE Homo sapiens EST sequence
JOURNAL Unpublished (2002)
COMMENT Contact: The Sanger Centre
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquerry@sanger.ac.uk
Sanger Centre name : scd10827.dT
Homo sapiens EST sequence. This sequence was generated as part of
The Wellcome Trust Sanger Institute program to identify and
annotate genes in the human genome. Incomplete or unconfirmed genes
are experimentally analysed using a variety of cDNA library
resources. This sequence was obtained from a PCR product generated
from a pool of up to 100,000 cDNA clones derived from
pool_YT_11b_v_SPD cDNA library. Further information can be found at
http://www.sanger.ac.uk/Teams/Team69/.

FEATURES
source
1..599
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20"
/clone_11b="pool_YT_11b_v_SPD"
/note="Organ: Breast; Vector: pZERO-1; Site 1: SphI;
Site 2: SphI; Ductal carcinoma in situ, high-grade, comedo
, from 41 yo female. Library constructed in the laboratory
of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."
```

BASE COUNT 142 a 148 c 165 g 144 t

ORIGIN

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Query Match 20.0%; Score 513; DB 9; Length 599;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1994 TAAATTTTGTATTTTATAGACATGGGTTTACACATTTGGCCAGGCTGTGTCA 2053
Db 520 TAAATTTTGTATTTTATAGACATGGGTTTACACATTTGGCCAGGCTGTGTCA 461

Oy 2054 ACTCTGACCTAGTGATCCACCACTTGGCTCCCAAGGCTGGGATTAAGGTG 2113
Db 460 ACTCTGACCTAGTGATCCACCACTTGGCTCCCAAGGCTGGGATTAAGGTG 401

Oy 2114 GAGCAGGCAACCCAGGCTAGCTCAGATCTCAATTTATTTTGGCTTACCATTTCC 2173
Db 400 GAGCAGGCAACCCAGGCTAGCTCAGATCTCAATTTATTTTGGCTTACCATTTCC 341
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QY 2174 TAGCACTGGCTTGGCCATCTTGTGGCCGATAAATAACACCTCTTAAGCTTAGCA 2233
 DB 340 TAGCACTGGCTTGGCCATCTTGTGGCCGATAAATAAACAACCTCTTAAGCTTAGCA 281
 QY 2234 CACTGAGTGAAGCCAGGACCTCACTGCTGGGAGGGGATCAGAAAGTCTTAAGCCCT 2293
 DB 280 CACTGAGTGAAGCCAGGACCTCACTGCTGGGAGGGGATCAGAAAGTCTTAAGCCCT 221
 QY 2294 CTCTCCAGATGCCAAGAGAGACCAAGGCTCAACCAATTCAGCCCTTAATTCCT 2353
 DB 220 CTCTCCAGATGCCAAGAGAGACCAAGGCTCAACCAATTCAGCCCTTAATTCCT 161
 QY 2354 GCTGCTCCATTAACAGAAAGAGTCTGCTGATCCGCTTAAGGATCGAGAGAGAGA 2413
 DB 160 GCTGCTCCATTAACAGAAAGAGTCTGCTGATCCGCTTAAGGATCGAGAGAGAGA 101
 QY 2414 AAGAGGATGGGGTGGAGAGCCCTCCAGTCTCTTAAGGATCGAGAGAGAGA 2473
 DB 100 AAGAGGATGGGGTGGAGAGCCCTCCAGTCTCTTAAGGATCGAGAGAGAGA 41
 QY 2474 GGGGTGGAAAGCTTTATCAGGTATCATCAAC 2506
 DB 40 GGGGTGGAAAGCTTTATCAGGTATCATCAAC 8

RESULT 12
 BG284179 566 bp mRNA linear EST 21-FEB-2001
 LOCUS 602408226F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4520382 5',
 mRNA sequence.
 ACCESSION BG284179
 VERSION BG284179
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 AUTHORS NIH-MGC http://mgi.mcl.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: rgs@nih.gov
 Tissue Procurement: DCT/DTP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LNL0418 row: c column: 07
 High quality sequence start: 2
 High quality sequence stop: 566.
 Location/Qualifiers

FEATURES
 source 1..566

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4520382"
 /clone_1ib="NIH_MGC_91"
 /tissue_type="adenoecarcinoma, cell line"
 /lab_host="DH10B (phage-restant)"
 /note="Organ: prostate; Vector: pCMV-SPORT6; Site: 1: NotI;
 Site: 2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.4 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: This is a NIH_MGC library."
 BASE COUNT 116 a 187 c 152 g 110 t 1 others
 ORIGIN

Query Match 19.0%; Score 488; DB 12; Length 566;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 796 GGGCTTTACTCTCTGCACTCCGCTCAGCCGCTTCTGGAGCGGATCAGAC 855
 DB 13 GGGCTTTACTCTCTGCACTCCGCTCAGCCGCTTCTGGAGCGGATCAGAC 72
 QY 856 TACAGATTCACAGCTGCTTACATAGCTGATCATTCACGCGCTCAGCTTCC 915
 DB 73 TACAGATTCACAGCTGCTTACATAGCTGATCATTCACGCGCTCAGCTTCC 132
 QY 916 TACTTCAGGCGCTGGTGGACATTAATCTGAGCTGGGATGACATCTGCTTCT 975
 DB 133 TACTTCAGGCGCTGGTGGACATTAATCTGAGCTGGGATGACATCTGCTTCT 192
 QY 976 AAGAGCCCTGTCTCTGAGAGGAGCTGAGCCGCTCCCTGCAAGATATACCTTACT 1035
 DB 193 AAGAGCCCTGTCTCTGAGAGGAGCTGAGCCGCTCCCTGCAAGATATACCTTACT 252
 QY 1036 GTGACTGTGAGAGGACACATCTCACTGAGAAAGCTGAGACCTTCTTCTTCT 1095
 DB 253 GTGACTGTGAGAGGACACATCTCACTGAGAAAGCTGAGACCTTCTTCTTCT 312
 QY 1096 GAGCTGCAAGAGGAGAGCTCTTCTCAGTGAAGGCTCCGAGAGTCCCTCAGCTTC 1155
 DB 313 GAGCTGCAAGAGGAGAGCTCTTCTCAGTGAAGGCTCCGAGAGTCCCTCAGCTTC 372
 QY 1156 TACATCAGCTGATGATGACAGGCTCTCTTTGATGATGCTAGGCCCAAGAGAGGC 1215
 DB 373 TACATCAGCTGATGATGACAGGCTCTCTTTGATGATGCTAGGCCCAAGAGAGGC 432
 QY 1216 CAAGAGGAAACCAAGCTGACACCTAGAACCCCAATTCAGCTCTGAGGACCCAG 1275
 DB 433 CAAGAGGAAACCAAGCTGACACCTAGAACCCCAATTCAGCTCTGAGGACCCAG 492
 QY 1276 GGCAAGGC 1283
 DB 493 GGCAAGGC 500

RESULT 13
 AL844311 597 bp mRNA linear EST 30-JUL-2002
 LOCUS AL844311 pool_YT_11b_v_SPD Homo sapiens cDNA, mRNA sequence.
 DEFINITION AL844311
 ACCESSION AL844311
 VERSION AL844311.1 GI:22019093
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 AUTHORS Ashcroft, K., Betnel, G., Bye, J.M., Howell, G.R., Huckle, E.J. and
 Sheridan, E.
 TITLE Homo sapiens EST sequence
 JOURNAL Unpublished (2002)
 COMMENT Contact: The Sanger Centre
 The Sanger Centre
 Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: humeny@sanger.ac.uk
 Sanger Centre name: scc10818.154136A
 Homo sapiens EST sequence. This sequence was generated as part of
 The Wellcome Trust Sanger Institute program to identify and
 annotate genes in the human genome. Incomplete or unconfirmed genes
 are experimentally analysed using a variety of cDNA library
 resources. This sequence was obtained from a PCR product generated
 from a pool of up to 100,000 cDNA clones derived from
 pool YT_11b v SPD cDNA library. Further information can be found at
 http://www.sanger.ac.uk/teams/team69/.

FEATURES
 source 1..597

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /map="20"
 /clone_1ib="pool YT_11b v SPD"
 /note="Organ: breast; Vector: pZero-1; Site: 1: SphI;

AUTHORS

Ashcroft, K., Bethel, G., Bye, J.M., Howell, G.R., Huckle, E.J. and Sheridan, E.

TITLE

Homo sapiens EST sequence
Unpublished (2002)

JOURNAL

Contact: The Sanger Centre
The Sanger Centre

COMMENT

Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquery@sanger.ac.uk
Sanger Centre name: sccid10817.4004898
Homo sapiens EST sequence. This sequence was generated as part of The Wellcome Trust Sanger Institute program to identify and annotate genes in the human genome. Incomplete or unconfirmed genes are experimentally analysed using a variety of cDNA library resources. This sequence was obtained from a PCR product generated from a pool of up to 100,000 cDNA clones derived from pool FLU 11b v SPC cDNA library. Further information can be found at <http://www.sanger.ac.uk/Teams/Team69/>.

FEATURES

source

1. .611
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/db_xref="taxon:9606"
/map="20"
/clone_lib="pool FLU 11b v SPC"
/note="Organ: breast; Vector: pZERO-1; Site: 1: SpH1;
Site 2: SpH1; Ductal carcinoma in situ, high grade, comedo
, from 41 yo female. Library constructed in the laboratory
of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."

BASE COUNT

132 a 157 c 173 g 149 t

ORIGIN

Query Match 17.7%; Score 454; DB 9; Length 611;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 504; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1095 TGAAGCTGCCACAGGGAGAGTCTTCTCACTGAGGCTCTCCGAGTCTCTCACTT 1154
DB 577 TGAAGCTGCCACAGGGAGAGTCTTCTCACTGAGGCTCTCCGAGTCTCTCACTT 518
OY 1155 CTACATCAAGCTGGAATGACAGGCTGTCTTTGGATGATGCTTGGCCCAAAGAGAGG 1214
DB 517 CTACATCAAGCTGGAATGACAGGCTGTCTTTGGATGATGCTTGGCCCAAAGAGAGG 458
OY 1215 CCAAAAGGAAACCAAGGCTGCAACCTAGAAACCCCAATTCAGCTCTTGCGCAACCCAG 1274
DB 457 CCAAAAGGAAACCAAGGCTGCAACCTAGAAACCCCAATTCAGCTCTTGCGCAACCCAG 398
OY 1275 AGGCAAGGCTGTGCACTCAGGAGAGGAGTGGGACACAGAGGTGATCTAGAGTCCAC 1334
DB 397 AGGCAAGGCTGTGCACTCAGGAGAGGAGTGGGACACAGAGGTGATCTAGAGTCCAC 338
OY 1335 CTGTAACCTTCTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1394
DB 337 CTGTAACCTTCTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 278
OY 1395 TGATCCCACTGCACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1454
DB 277 TGATCCCACTGCACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 218
OY 1455 AAAAAGAGATTAAGCTCTCTGAGGAGTCTGACCTTCTTCTTCTTCTTCTTCTTCTT 1514
DB 217 AAAAAGAGATTAAGCTCTCTGAGGAGTCTGACCTTCTTCTTCTTCTTCTTCTTCTT 158
OY 1515 AGTACCATCTGGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1574
DB 157 AGTACCATCTGGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 98
OY 1575 CCCACCCAAAGGTAAACACCC 1599
DB 97 CCCACCCAAAGGTAAACACCC 73

RESULT 16
BP510664/c

LOCUS

BP510664 451 bp mRNA linear EST 06-DEC-2000
DEFINITION UI-H-814-acf-b-01-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone

ACCESSION

IMAGE:3084601.3', mRNA sequence.

VERSION

BP510664

KEYWORDS

BP510664.1 GI:11593962

SOURCE

EST.

ORGANISM

human.

REFERENCE

1 (bases 1 to 451)

AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

JOURNAL

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabp-remail@nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA library preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/ILNL at:
www-bio.lnl.gov/bbrp/image/image.html
Seq primer: M3 Forward
POLYA=Yes.

FEATURES

source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3084601"
/clone_lib="NCI CGAP Sub8"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; NCI CGAP Sub8
is a subcloned library derived from NCI CGAP Sub5. The
NCI CGAP Sub8 library had 2.5 million recombinants. A
single-stranded DNA preparation of NCI CGAP Sub5 was used
as a tracer in a subtractive hybridization with a driver
comprising a pool of clones from NCI CGAP Sub5 (IMAGE
clone ids 272833-2737415, 3068040-3069191; 25% of the
driver population), a pool of clones from NCI CGAP Sub4
(IMAGE clone ids 2723592-2729326; 25% of the driver
population), NCI CGAP Sub6 (pool AIF-AU, IMAGE ids
2728969-2733190; 25% of the driver population), and
NCI CGAP Sub7 (IMAGE ids 3069192-3072228, 3081864-3084550
; 25% of the driver population). Subtraction was
performed as previously described [Bonaldi, Lennon &
Soares (1996): Normalization and Subtraction: Two
Approaches To Facilitate Gene Discovery. Genome Research
6, 791-806.
TAG LIB=NCI CGAP Col0
TAG TISSUE=colon
TAG SEQ=AAACG"

BASE COUNT

97 a 110 c 115 g 129 t

Query Match 17.2%; Score 441; DB 12; Length 451;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2121 GGCACCCAGCTGCTCTCAGATCTATTTCTTGTGGCTTACATTCCTTACACACA 2180
DB 441 GGCACCCAGCTGCTCTCAGATCTATTTCTTGTGGCTTACATTCCTTACACACA 382
OY 2181 CTGGCTTGCATCTTGTGGCCGAATTAATTAACCTCTTAAGCTTGACACTGCA 2240
DB 381 CTGGCTTGCATCTTGTGGCCGAATTAATTAACCTCTTAAGCTTGACACTGCA 322
OY 2241 GTGAGGCCAGGACCTCAGTGTGGGCGAGGCGATCAGAAGTCTAAGCCCTCTCTCA 2300
DB 321 GTGAGGCCAGGACCTCAGTGTGGGCGAGGCGATCAGAAGTCTAAGCCCTCTCTCA 262


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/clone_lib="NCI_CGAP_Lym12"
/tissue_type="Lymphoma, follicular mixed small and large
cell"
/lab_host="DH10B"
/note="Organ: Lymph node; Vector: pCMV-SPORT6, Site 1:
Sali; Site 2: NotI; Cloned unidirectionally. Primer:
Oligo dt. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"

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BASE COUNT      94 a      100 c      109 g      106 t
ORIGIN
Query Match      15.9%; Score 409; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2127 CAGCCAGCTCTCAGATCTCTATTTGCTTACCTTCCCGACACCTGGCC 2186
Db 409 CAGCCAGCTCTCAGATCTCTATTTGCTTACCTTCCCGACACCTGGCC 350
Qy 2187 TTGCCATCTTGTGGCCGAAATATAACACCTTTAAGTCTAGCACACTGACGAG 2246
Db 349 TTGCCATCTTGTGGCCGAAATATAACACCTTTAAGTCTAGCACACTGACGAG 290
Qy 2247 CAGGACCTCAGTGTGGGCGAGGCGACATGAGAGCTTACCCCTCTCCACATGC 2306
Db 289 CAGGACCTCAGTGTGGGCGAGGCGACATGAGAGCTTACCCCTCTCCACATGC 230
Qy 2307 CAAGAAGAGACCAACAGCTTACCAAAATCCAGCCCTTGTCCCTGCTCCATTA 2366
Db 229 CAAGAAGAGACCAACAGCTTACCAAAATCCAGCCCTTGTCCCTGCTCCATTA 170
Qy 2367 ACAGAAAGAGGTCTGTGATTCGGCTAAGAGATAGAGAGAGAAAGAGAGATGGG 2426
Db 169 ACAGAAAGAGGTCTGTGATTCGGCTAAGAGATAGAGAGAGAAAGAGAGATGGG 110
Qy 2427 TGGAGGACACCCCTCCAGTCTCTCACTGCTTCCCAAGCTACAGTGGGTGGAAAG 2486
Db 109 TGGAGGACACCCCTCCAGTCTCTCACTGCTTCCCAAGCTACAGTGGGTGGAAAG 50
Qy 2487 CTTTATCAGGTATCATCAACAGGTCTCTCAATTAAAGTTTGAATTATTC 2535
Db 49 CTTTATCAGGTATCATCAACAGGTCTCTCAATTAAAGTTTGAATTATTC 1

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RESULT 19      397 bp      mRNA      linear      EST 16-OCT-2000
BF057252/c     7k18a03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:344389 3',
LOCUS          mRNA sequence.
DEFINITION     BFO57252
ACCESSION      BFO57252
VERSION        BFO57252.1 GI:10811148
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

```

REFERENCE      1 (bases 1 to 397)
AUTHORS       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE         National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                Tumor Gene Index
JOURNAL        Unpublished (1997)
COMMENT        Contact: Robert Strausberg, Ph.D.
                Email: c9abbs-r@mail.nih.gov
                Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
                R. Emmert-Buck, M.D., Ph.D.
                cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                Bonaldo, Ph.D.
                cDNA Library Arrayed by: Greg Lennon, Ph.D.
                DNA Sequencing by: Washington University Genome Sequencing Center
                Clone distribution: NCI-CGAP clone distribution information can be
                found through the I.M.A.G.E. Consortium/LML, send email to:
                info@image.llnl.gov
                Seq primer: -40UP from Gibco.

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FEATURES
source         Location/Qualifiers
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                /db_xref="taxon:9606"
                /clone="IMAGE:344389"
                /clone_lib="NCI_CGAP_GC6"
                /tissue_type="pooled germ cell tumors"
                /lab_host="DH10B"
                /note="Vector: pRT73D-Pac (pharmacia) with a modified
                polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
                from the normalized library NCI CGAP GC4 was prepared, and
                as circles were made in vitro. Following HAP purification,
                this DNA was used as tracer in a subtractive hybridization
                reaction. The driver was PCR-amplified cDNAs from a pool
                of 5,000 clones made from the same library (cloneids
                1257096-1258631, 1469064-1470983, and 1475592-1476743).
                Subtraction by Bento Soares and M. Fatima Bonaldo."

```

```

BASE COUNT      88 a      100 c      109 g      109 t
ORIGIN
Query Match      15.5%; Score 397; DB 12; Length 397;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2154 TTTTGTGCTTACCATCTTCCAGACACTGCTTCCATCTTGTGCGAATAAAAAT 2213
Db 397 TTTTGTGCTTACCATCTTCCAGACACTGCTTCCATCTTGTGCGAATAAAAAT 338
Qy 2214 AACACCTCTTAAGCTTACGACACTGAGGCGAGGACCTGAGTGTGGGCGAGGGG 2273
Db 337 AACACCTCTTAAGCTTACGACACTGAGGCGAGGACCTGAGTGTGGGCGAGGGG 278
Qy 2274 ATCAGAGGTGCTTAAGCCTCTCTCCAAATGCGAAGACGAGACACAGCTTACCCA 2333
Db 277 ATCAGAGGTGCTTAAGCCTCTCTCCAAATGCGAAGACGAGACACAGCTTACCCA 218
Qy 2334 ATCCAGCCTTGAATTTCCCTGCTCTCCATTAACGAAAGAGTGTGATCCGCTTA 2393
Db 217 ATCCAGCCTTGAATTTCCCTGCTCTCCATTAACGAAAGAGTGTGATCCGCTTA 158
Qy 2394 AGGATCAGGAGAGAGAGAGAGAGAGATGGGTGGAGAGCACCCTCCAGTCTCTTA 2453
Db 157 AGGATCAGGAGAGAGAGAGAGAGAGATGGGTGGAGAGCACCCTCCAGTCTCTTA 98
Qy 2454 CTGTGTCACAGCTACAGGTGGGTGGAAAGCTTTATCAGGTATCATCAACAGGTTCT 2513
Db 97 CTGTGTCACAGCTACAGGTGGGTGGAAAGCTTTATCAGGTATCATCAACAGGTTCT 38
Qy 2514 CAATTAAAGATTGATTATTTCAAGTATGTGAAAAA 2550
Db 37 CAATTAAAGATTGATTATTTCAAGTATGTGAAAAA 1

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RESULT 20      397 bp      mRNA      linear      EST 16-OCT-2000
BF062179/c     7k13e03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3481060 3',
LOCUS          mRNA sequence.
DEFINITION     BFO62179
ACCESSION      BFO62179
VERSION        BFO62179.1 GI:10821089
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

```

REFERENCE      1 (bases 1 to 397)
AUTHORS       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE         National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                Tumor Gene Index
JOURNAL        Unpublished (1997)
COMMENT        Contact: Robert Strausberg, Ph.D.
                Email: c9abbs-r@mail.nih.gov
                Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

```

R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bernaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL. send email to: info@image.llnl.gov
 Seq primer: -400P from Gibco.

FEATURES

source
 1. .397
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3481060"
 /clone_1lb="NCI CCAP GC6"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI CCAP GC4 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bernaldo. "
 BASE COUNT 88 a 100 c 100 g 109 t
 ORIGIN

Query Match 15.5%; Score 397; DB 12; Length 397;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2154 TTTTGGGCTTACCATTCCTAGACACTGCGCTTGCATTTGTGGCCGATAAATAAT 2213
 Db 397 TTTTGGGCTTACCATTCCTAGACACTGCGCTTGCATTTGTGGCCGATAAATAAT 338
 QY 2214 AACACCTCTTAAGTCTAGACACTGCGAGGAGGACCTGAGTGGGAGGAGC 2273
 Db 337 AACACCTCTTAAGTCTAGACACTGCGAGGAGGACCTGAGTGGGAGGAGC 278
 QY 2274 ATCAGAGGCTCAAGCCCTCTCCCAATGCGAGAGGAGCCAGCCCTACACCA 2333
 Db 277 ATCAGAGGCTCAAGCCCTCTCTCCCAATGCGAGAGGAGCCAGCCCTACACCA 218
 QY 2334 ATCCAGCCCTTGAATTCCTGCTCTCCATTAACAGAAAGGCTGCTGATCCGCTA 2393
 Db 217 ATCCAGCCCTTGAATTCCTGCTCTCCATTAACAGAAAGGCTGCTGATCCGCTA 158
 QY 2394 AGGATCAGAGGAG 2453
 Db 157 AGGATCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 98
 QY 2454 CTGGTCCCAAGCTACAGTGGGGTGGGAAAGGCTTTATCAGATATCAACAGTTCT 2513
 Db 97 CTGGTCCCAAGCTACAGTGGGGTGGGAAAGGCTTTATCAGATATCAACAGTTCT 38
 QY 2514 CAATTAAAGATTGATTATTCAGTATGTGAAAAA 2550
 Db 37 CAATTAAAGATTGATTATTCAGTATGTGAAAAA 1

RESULT 21

BO053486 878 bp mRNA linear EST 29-MAR-2002
 LOCUS BO053486
 DEFINITION AGENCOURT 6822017 NIH_MGC_106 Homo sapiens CDNA IMAGE:5935253
 5' mRNA sequence.
 ACCESSION BO053486
 VERSION BO053486.1 GI:19812826
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 878)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: sgabbs-remail.nih.gov
 Tissue Procurement: Dr. Daniel McVicar, DMS/NCI
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 plate: LUCM2122 row: 1 column: 06
 High quality sequence stop: 394.

FEATURES

source
 1. .878
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5935253"
 /clone_1lb="NIH MGC 106"
 /tissue_type="natural killer cells, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: blood; Vector: pT73D-Pac; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
 BASE COUNT 201 a 253 c 233 g 190 t 1 others
 ORIGIN

Query Match 15.2%; Score 390; DB 14; Length 878;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 196 CTACCCAAACCAACCTAGACCTCTCCGAAAGTCTCCCAAGGCTGAGAGATTCTGGG 255
 Db 54 CTACCCAAACCAACCTAGACCTCTCCGAAAGTCTCCCAAGGCTGAGAGATTCTGGG 113
 QY 256 TGTCTTAGACCAAGAGCACTGGCAGACTTCCAGAGAGGCCCCCAAGCCTTAACCTGTC 315
 Db 114 TGTCTTAGACCAAGAGCACTGGCAGACTTCCAGAGAGGCCCCCAAGCCTTAACCTGTC 173
 QY 316 CAGCAGACATGAGTCTCAGAGAGCTGTCTCCCAAGGCTTGAATGACAAACCAATT 375
 Db 174 CAGCAGACATGAGTCTCAGAGAGCTGTCTCCCAAGGCTTGAATGACAAACCAATT 233
 QY 376 CCTCGATGATGTGCTTGAATGCTCTGCTGAGAGAAACATGGAAAGTCTCCAGAGAA 435
 Db 234 CCTCGATGATGTGCTTGAATGCTCTGCTGAGAGAAACATGGAAAGTCTCCAGAGAA 293
 QY 436 AGAAATCTCTGCAAGCCCAAGCTTGAATCTCTCTCCCAAGGCTGAGAGAGCTGTAGC 495
 Db 294 AGAAATCTCTGCAAGCCCAAGCTTGAATCTCTCTCCCAAGGCTGAGAGAGCTGTAGC 353
 QY 496 ATGGAAGCAGAGAGAGCAAGGCAAGCCTGAGGCTCTGGGAGCTTCCCGGAGGTGGC 555
 Db 354 ATGGAAGCAGAGAGAGCAAGGCAAGCCTGAGGCTCTGGGAGCTTCCCGGAGGTGGC 413
 QY 556 CCGGCGAGCTGTGCTGAGAGCTGGGAGGAGCATTTGATGCTCTGAGAGTGAAGAC 615
 Db 414 CCGGCGAGCTGTGCTGAGAGCTGGGAGGAGCATTTGATGCTCTGAGAGTGAAGAC 473
 QY 616 TGGTGAACGGTGTCTGTGA 636
 Db 474 TGGTGAACGGTGTCTGTGA 494

RESULT 22

A1476150/c A1476150 301 bp mRNA linear EST 09-MAR-1999
 LOCUS tnc2f01.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2174137 3',
 DEFINITION mRNA sequence.
 ACCESSION A1476150
 VERSION A1476150.1 GI:4329184
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 301)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapdb-remail.nih.gov
 Life Technologies catalog #: 11547-015
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 www-bio.linn.gov/bbrp/image/image.html
 Seg primer: -40UP from Gibco
 High quality sequence stop: 283.
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 /db_xref="taxon:9606"
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 cell"
 /lab_host="DH10B"
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 Salt; Site_2: NotI; Cloned unidirectionally. Primer:
 Oligo dt. Average insert size 1.25 kb. Life Technologies
 catalog #: 11547-015"
 BASE COUNT 61 a 84 c 77 g 79 t
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 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2235 ACTGCAGTGAAGCCAGGCACTCAGTGTGGGAGGGGATCAGAGGTCCTAAGCCTC 2294
 Db 301 ACTGCAGTGAAGCCAGGCACTCAGTGTGGGAGGGGATCAGAGGTCCTAAGCCTC 242
 QY 2295 TCTCCAAATGCCAAGCAGAGACACAGCTTACCAATCCAGCCTGATTTCCCTG 2354
 Db 241 TCTCCAAATGCCAAGCAGAGACACAGCTTACCAATCCAGCCTGATTTCCCTG 182
 QY 2355 CTGGCTCCATTAACAGAAAGAGTCTGCTGATCCGTAAGGATCAGGAGAGAA 2414
 Db 181 CTGGCTCCATTAACAGAAAGAGTCTGCTGATCCGTAAGGATCAGGAGAGAA 122
 QY 2415 AAGAGGATGGGTTGGAGGACCCCTCAATGCTCTACTGTTCCCAAGCTACAGTG 2474
 Db 121 AAGAGGATGGGTTGGAGGACCCCTCAATGCTCTACTGTTCCCAAGCTACAGTG 62
 QY 2475 GGGTGGAAAGCTTTATCAGGATCATCAACAGTTCTCAATTAAGATTGTTATT 2534
 Db 61 GGGTGGAAAGCTTTATCAGGATCATCAACAGTTCTCAATTAAGATTGTTATT 2
 QY 2535 C 2535
 Db 1 C 1
 RESULT 23
 BF059756/c 397 bp mRNA linear EST 16-OCT-2000
 LOCUS BF059756

DEFINITION 7k65h11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3480452 3',
 LOCUS tnc2f01.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3480452 3',
 mRNA sequence.
 ACCESSION BF059756
 VERSION BF059756.1 GI:10813652
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 397)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapdb-remail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL, send email to:
 Info@image.linn.gov
 Seg primer: -40UP from Gibco.
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3480452"
 /clone_lib="NCI CGAP GC6"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
 from the normalized library NCI CGAP GC4 was prepared, and
 ss circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones IDs
 157096-1258531, 1469064-1470983, and 1475592-1476743).
 Subtraction by Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 89 a 99 c 110 t
 ORIGIN
 Query Match 11.5%; Score 295; DB 12; Length 397;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2154 TTTGTGGCTTACCATTCCTAGACACTGGCTTGCATCTTGTGGCCGATTAATAAT 2213
 Db 397 TTTGTGGCTTACCATTCCTAGACACTGGCTTGCATCTTGTGGCCGATTAATAAT 338
 QY 2214 AACACCTTAACTAGACACTGAGGAGGAGGACCTGAGTGGGAGGGG 2273
 Db 337 AACACCTTAACTAGACACTGAGGAGGAGGACCTGAGTGGGAGGGG 278
 QY 2274 ATCAGAGGTGCTTAAGCCCTCTTCCAAATGCCAAGCAGACCACTACCA 2333
 Db 277 ATCAGAGGTGCTTAAGCCCTCTTCCAAATGCCAAGCAGACCACTACCA 218
 QY 2334 ATCAGAGCTTGAATTTCCCTGCTGCTCCATTAAGAGAGTGTGGATCCGCTA 2393
 Db 217 ATCAGAGCTTGAATTTCCCTGCTGCTCCATTAAGAGAGTGTGGATCCGCTA 158
 QY 2394 AAGGATCAGGAGAGAGAGAGAGAGTGGGTGGAGGACCCCTCCAGTCTCTTA 2453
 Db 157 AAGGATCAGGAGAGAGAGAGAGAGTGGGTGGAGGACCCCTCCAGTCTCTTA 98
 QY 2454 CTGGTCCCAAGTACAGGTGGGAGAGAGCTTTATCAGGATCATCAACAGTTCT 2513
 Db 97 CTGGTCCCAAGTACAGGTGGGAGAGAGCTTTATCAGGATCATCAACAGTTCT 38


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QY 2514 CATTAAAGATTGATTATTCAAGATGTGAAAAA 2550
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Db 37 CATTAAAGATTGATTATTCAAGATGTGAAAAA 1
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RESULT 24
BG25545

LOCUS	6255345	522 bp	mRNA	linear	EST I3-FEB-2001
DEFINITION	602367806F1 NIH_MGC_91 Homo sapiens CDNA clone IMAGE:4476049 5',				
ACCESSION	BC355445				
	mRNA sequence.				

ACCESSION	D923742
VERSION	BC255445.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

FEATURES	COMMENT
AUTHORS	NIH-MGC
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
	Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.
	Email: cgapbs-rc@mail.nih.gov
	Tissue Procurement: DCTD/DRP
	cDNA Library Preparation: Life Technologies, Inc.
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLW)
	DNA Sequencing by: Incyte Genomics, Inc.
	Clone distribution: MGC Clone distribution information can be
	found through the I.M.A.G.E. Consortium/LNLW at:
	http://image.llnl.gov
	Plate: LLAM10302 row: 1 column: 02
	High quality sequence scop: 522.
	Location/Qualifiers

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1. .522
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/db xref="taxon:9606"
/cdn="IMAGE:4476049"
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/tissue_type="adenocarcinoma, cell line"
/lab_host="DHIO (phage-resistant)"
/note="Organ: prostate; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; cloned unidirectionally; oligo-dT primed. Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC library."
BASE COUNT
126 a 146 c 121 g 129 t
ORIGIN

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	Query Match	10.2%	Score 262;	DB 12;	Length 522;
	Best Local Similarity	99.7%	Pred. No. 0;		
	Matches 382;	Conservative	0;	Mismatches	0; Indels 1; Gaps 1;
Qy	1617	GCATTTTCAGAAAATCTACAGCTCTCTTGAGACACACCATCTCCAGAAAGTTAGA	1676		
Db	1	GCATTTTCAGAAAATCTACAGCTCTCTTGAGACACACCATCTCCAGAAAGTTAGA	60		
Qy	1677	CTGTGGCTTGAAAGGAGAAAGTGAATGATGTTCTTACCTGACGACGATCTTGG	1736		
Db	61	CTGTGGCTTGAAAGGAGAAAGTGAATGATGTTCTTACCTGAGACGACATCTTGG	120		
Qy	1737	ATGTGTCCAGGCTCTATGTGACCTTCAGAACCAAGAGAAAGTCTGGACAGTGTAGTTC	1796		
Db	121	ATGTGTCCAGGCTCTATGTGACCTTCAGAACCAAGAGAAAGTCTGGACAGTGTAGTTC	180		
Qy	1797	TGAATGTGTCCCATTTGAGAGCAACAGGCCCGAGCTTTTCTTTTTTTTGGAGCGAG	1856		
Db	181	TGAATGTGTCCCATTTGAGAGCAACAGGCCCGAGCTTTTCTTTTTTTTGGAGCGAG	239		
Qy	1857	TTCTGCTCTGTGTCCCATGTCTGGAGTGTCAATGGACGATCTCAGCTCAACCTTCA	1916		
Db	240	TTCTGCTCTGTGTCCCATGTCTGGAGTGTCAATGGACGATCTCAGCTCAACCTTCA	299		

Accession	Sequence	Length
Oy	TCCTCGATTTAAACAAATCTCTCTGCTCAGCTCCAGAAATGCTGATTAAGAGCT	1976
Oy	1917	
Db	TCCTCGATTTAAACAAATCTCTCTGCTCAGCTCCAGAAATGCTGATTAAGAGCGT	359
Db	300	
Oy	ACACGACATGCTGCTAAATTT	1999
Oy	1977	
Db	ACACGACATGCTGCTAAATTT	382
Db	360	

RESULT 25	
AL844309	AL844309 606 bp mRNA linear EST 30-JUL-2002
LOCUS	
DEFINITION	AL844309 pool_FUJ_1ib_v_SPC Homo sapiens CDNF, mRNA sequence.
ACCESSION	AL844309
VERSION	AL844309.1 GI:22019091

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

[illegible]

TITLE Homo sapiens EST sequence
JOURNAL Unpublished (2002)
COMMENT Contact: The Sanger Centre
 The Sanger Centre
 Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: humguery@sanger.ac.uk
 Sanger Centre name : scdd10817.154136A
 Homo sapiens EST sequence. This sequence was generated as part of
 The Wellcome Trust Sanger Institute program to identify and
 annotate genes in the human genome. Incomplete or unconfirmed genes
 are experimentally analysed using a variety of cDNA library
 resources. This sequence was obtained from a PCR product generated
 from a pool of up to 100,000 cDNA clones derived from
 pool FLU lib v SPC cDNA library. Further information can be found
 at <http://www.sanger.ac.uk/Teams/Team69/>.

FEATURES	LOCATION/VARIABLES
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	/db xref="taxon:9606"
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	/note="Organ: breast; Vector: pZEVO-1, Site_1: SphI,
	Site_2: SphI; Ductal carcinoma in situ, high-grade, Comedo
	, from 41 yo Female. Library constructed in the laboratory
	of K. Polyak, M.D., Ph.D. (Dana-Farber Cancer Institute)."
BASE COUNT	138 a 186 c 154 g 125 t 3 others
ORIGIN	

Query Match	9.64	Score 247	DB 9	Length 606
Best Local Similarity	99.44	Pred. No. 0		
Matches 347	Conservative	0	Mismatches 2	Indels 0
				Gaps 0
Oy	925	GGCCGTGTGACCATTA	CTGTGAGCTGGGGGATACAT	TGCTGCTACTACAAAGAGCC 984
Db	46	GGCCGTGTGACCATTA	CTGTGAGCTGGGGGATACAT	TGCTGCTACTACAAAGAGCC 105
Oy	985	TGTGTCCGTGAGAGG	AGCTGGCCGCTCCCTGTGGCAAGGATAT	ACCCTCACTGTGACTGTG 1044
Db	106	TGTGTCCGTGAGAGG	AGCTGGCCGCTCCCTGTGGCAAGGATAT	ACCCTCACTGTGACTGTG 165
Oy	1045	CAGAGGACACACT	CACTGAAGGAGCTGAGACAGCTCCCTCGTTT	TTGTGAAGCTGCC 1104
Db	166	CAGAGGACACACT	CACTGAAGGAGCTGAGACAGCTCCCTCGTTT	TTGTGAAGCTGCC 225
Oy	1105	ACAGGGAGAGAGT	CTCTTCTTAAGTGAAGGCTTCCGGAGATCCCT	CACTTCAATCAAGC 1164
Db	226	ACAGGGAGAGAGT	CTCTTCTTAAGTGAAGGCTTCCGGAGATCCCT	CACTTCAATCAAGC 285
Oy	1165	CTGAATGACAGAGCT	GTCTCTTTTGATGATGATCCAGAGCCCAAGAGAGG	CCCAAAAGGA 1224

mRNA sequence.
 ACCESSION A1002059
 VERSION A1002059.1 GI:3202096
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 110)
 AUTHORS NC-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NC-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www-bio.lnlnl.gov/bdip/image/image.html
 Seq primer: -40m13 fwd. RT from Amersham.
 Location/Qualifiers
 1..110
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1613268"
 /clone_1ib="NCI CGAP GC3"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
 BASE COUNT 28 a 21 c 15 g 46 t
 ORIGIN
 Query Match 3.5%; Score 90; DB 9; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2451 CTACTGGTCCAGCTACAGTGGGTGGGAAAGCTTTATCAGATCATCAACAGGT 2510
 DB 110 CTACTGGTCCAGCTACAGTGGGTGGGAAAGCTTTATCAGATCATCAACAGGT 51
 QY 2511 TCTCAATTAAAGATTGATTATTATTCAGTA 2540
 DB 50 TCTCAATTAAAGATTGATTATTATTCAGTA 21
 RESULT 29
 LOCUS AA309769 149 bp mRNA linear EST 19-APR-1997
 DEFINITION EST180699 Jurkat T-cells V Homo sapiens cDNA 5' end, mRNA sequence.
 ACCESSION AA309769
 VERSION AA309769.1 GI:1962171
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 149)
 AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fulmer, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Well, C., Clayson, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, J.M., Fitch, W.M., Fitchman, D.L., Geoghegan, N.S., Glick, A.,

Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr., Kelley, J.M., Kelley, J.C., Liu, L.-T., Marmaro, S.M., Merrick, J.M., Moreno-Palancas, R.F., McDonald, L.A., Nguyen, D.T., Bellierino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudak, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utecht, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hung, J., Li, H., Weisner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wang, J., Xu, C., Yu, G., Ruden, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
 TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
 JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
 MEDLINE 9606280
 COMMENT Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerv@tigr.org
 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.
 Location/Qualifiers
 1..149
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /db_xref="ATCC (inhost):155929"
 /clone_1ib="Jurkat T-cells v"
 /cell_type="T-lymphocyte"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI"
 BASE COUNT 38 a 46 c 36 g 27 t 2 others
 ORIGIN
 Query Match 3.0%; Score 76; DB 9; Length 149;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1217 AAAAGGAAACCAAGGCTGCACACTAGACCCCAATTCAGCTCTGGGACCCAGAG 1276
 DB 74 AAAAGGAAACCAAGGCTGCACACTAGACCCCAATTCAGCTCTGGGACCCAGAG 133
 QY 1277 GCAAGGCTGTGACCTC 1292
 DB 134 GCAAGGCTGTGACCTC 149
 RESULT 30
 LOCUS AQ341462 489 bp DNA linear GSS 06-MAY-1999
 DEFINITION RPII11-11111.TV RPII-11 Homo sapiens genomic clone RPII-11-111111, DNA sequence.
 ACCESSION AQ341462
 VERSION AQ341462.1 GI:4163358
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 489)
 AUTHORS Zhao, S., Adams, M.D., Niernan, W., Malek, J., de Jong, P. and Venter, J.C.
 TITLE Use of BAC End Sequences from Library RPII-11 for Sequence-Ready Map Building
 JOURNAL Unpublished (1997)
 COMMENT Other GSSs: RPII11-11111.TV
 Contact: Shaying Zhao, William Niernan, Mark Adams
 Department of Eukaryotic Genomics

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208

Email: hbe@tigr.org
Clones are derived from the human BAC library RPCT-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/cdb/human/bac_end_search.html
Seq primer: T7
Class: BAC ends.

FEATURES

source
1. .489
/organism="Homo sapiens"
/db_xref="GDB:7542514"
/db_xref="taxon:9606"
/clone_name="RPCT-11-111111"
/clone_id="RPCT-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; RPCT11 Human Male BAC Library"
BASE COUNT 140 a 100 c 102 g 147 t
ORIGIN

Query Match 2.9%; Score 74; DB 17; Length 489;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2035 TTGGCCAGGCTGTGTGGAACCTGACCTGATGATCCACCACTTGCCCTCCCAA 2094
DB 372 TTGGCCAGGCTGTGTGGAACCTGACCTGATGATCCACCACTTGCCCTCCCAA 313
QY 2095 GTGCTGGGATTACA 2108
DB 312 GTGCTGGGATTACA 299

RESULT 31
LOCUS A0431946 534 bp DNA linear GSS 31-MAR-1999
DEFINITION HS_5065_A2_F08_T7A RPCT-11 Human Male BAC Library Homo sapiens
ACCESSION A0431946
VERSION A0431946.1 GI:4542281
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCT-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu

Plate: 641 row: K column: 16
Seq primer: T7
Class: BAC ends
High quality sequence stop: 534.
Location/Qualifiers
1. .534

FEATURES

source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_name="Plate641 COL-16 Row=K"
/clone_id="RPCT-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"
BASE COUNT 144 a 105 c 119 g 155 t 11 others
ORIGIN

Query Match 2.9%; Score 74; DB 17; Length 534;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2035 TTGGCCAGGCTGTGTGGAACCTGACCTGATGATCCACCACTTGCCCTCCCAA 2094
DB 401 TTGGCCAGGCTGTGTGGAACCTGACCTGATGATCCACCACTTGCCCTCCCAA 342
QY 2095 GTGCTGGGATTACA 2108
DB 341 GTGCTGGGATTACA 328

RESULT 32
LOCUS BG943550 572 bp mRNA linear EST 11-JUN-2001
DEFINITION ax39b11.x1 Proliferating Human Erythroid Cells (LCB:ax library)
ACCESSION BG943550
VERSION BG943550.1 GI:14342922
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS Gubdin,A.N., Njoroge,J.M., Bouffard,G.G. and Miller,J.L.
TITLE Gene expression in proliferating human erythroid cells
JOURNAL Genomics 59 (2), 168-177 (1999)
MEDLINE 99339981
COMMENT Contact: Jeffery L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda, MD 20892, USA
Tel: 301 402 2373
Fax: 301 435 5148
Email: jml7@nih.gov

DNA Sequencing and analyses by National Institutes of Health Intramural Sequencing Center (NISC).
Plate: 39 row: D column: 11
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
1. .572

FEATURES

source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_name="ax39b11"
/clone_id="Proliferating Human Erythroid Cells (LCB:ax library)"
/sex="unknown"
/tissue_type="blood"
/cell_type="Erythroid Cells"
/cell_line="Primary Culture of Peripheral Blood Mononuclear Cells"

mRNA sequence.
 BE904397
 VERSION BE904397.1 GI:10396608
 EST.
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 737)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Plate: L1M9694 row: 1 column: 04
 High quality sequence stop: 673.
 Location/Qualifiers
 1..737
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3898443"
 /clone_1ib="NIH MGC 70"
 /tissue_type="epitheloid carcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: pancreas; Vector: pCMV-SPORT6; Site: 1; NCI; Site: 2; Salt; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.1 Kb. Library constructed by Life Technologies."

BASE COUNT 162 a 187 c 196 g 192 t
 ORIGIN

Query Match 2.8%; Score 71; DB 12; Length 737;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2050 TCGAATCTGACCTGAGTATCACCACCTGCTCCCAAGTGTGGATTACAG 2109
 DB 216 TCGAATCTGACCTGAGTATCACCACCTGCTCCCAAGTGTGGATTACAG 275
 QY 2110 GTGTGAGCCAC 2120
 DB 276 GTGTGAGCCAC 286

RESULT 38
 BE664472 832 bp mRNA linear EST 21-DEC-2000
 LOCUS 602146234P1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4309876 5',
 DEFINITION mRNA sequence.
 ACCESSION BE664472
 VERSION BE664472
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 832)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Plate: L1CM1183 row: p column: 05
 High quality sequence stop: 679.
 Location/Qualifiers
 1..832
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4309876"
 /clone_1ib="NIH MGC 48"
 /tissue_type="Primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: B-cells; Vector: pOTB7; Site: 1; XhoI; Site: 2; EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 168 a 221 c 228 g 215 t
 ORIGIN

Query Match 2.8%; Score 71; DB 12; Length 832;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2050 TCGAATCTGACCTGAGTATCACCACCTGCTCCCAAGTGTGGATTACAG 2109
 DB 253 TCGAATCTGACCTGAGTATCACCACCTGCTCCCAAGTGTGGATTACAG 312
 QY 2110 GTGTGAGCCAC 2120
 DB 313 GTGTGAGCCAC 323

RESULT 39
 BE758454 896 bp mRNA linear EST 15-MAY-2001
 LOCUS 60212853P1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4853076 5',
 DEFINITION mRNA sequence.
 ACCESSION BE758454
 VERSION BE758454.1 GI:14069107
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 896)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Plate: L1CM1698 row: 1 column: 13
 High quality sequence stop: 733.
 Location/Qualifiers
 1..896
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4853076"
 /clone_1ib="NIH MGC 48"
 /tissue_type="Primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"

/note="Organ: B-cells; Vector: pOTB7, Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCGAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

BASE COUNT 206 a 219 c 240 g 231 t

ORIGIN

Query Match 2.8%; Score 71; DB 12; Length 896;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2050 TCGAAGCTCTGACCTGAGGTGATCCACCACCTTGCTCCCAAGTCTGGGATTACAG 2109
Db 257 TCGAAGCTCTGACCTGAGGTGATCCACCACCTTGCTCCCAAGTCTGGGATTACAG 316
Qy 2110 GTGTGAGCCAC 2120
Db 317 GTGTGAGCCAC 327

RESULT 40
A0261419/c 581 bp DNA linear GSS 24-OCT-1998
LOCUS A0261419
DEFINITION CITBI-EI-2509P17.TF CITBI-EI Homo sapiens genomic clone 2509P17,
DNA sequence.
ACCESSION A0261419
VERSION A0261419.1 GI:3787943
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 581)
ADAMS, M.D., ROUNSELEY, S.D., ZHAO, S., BASS, S., LINHER, K., GOLDEN, K.,
BERRY, K., GRANGER, D., SUB, E., WIBLE, C., SHIZUYA, H., SIMON, M. and
VENTER, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
Unpublished (1998)
JOURNAL Other GSSs: CITBI-EI-2509P17.TR
COMMENT Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@igir.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES
source
1..581
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="2509P17"
/clone_1id="CITBI-EI"
/sex="male"
/cell_type="sperm"
/note="Vector: pBeloba11, Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"
BASE COUNT 180 a 131 c 151 g 119 t
ORIGIN

Query Match 2.7%; Score 69; DB 17; Length 581;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2052 GAATCTCTGACCTGAGGTGATCCACCACCTTGCCCTCCCAAGTCTGGATTACAGT 2111
Db 511 GAATCTCTGACCTGAGGTGATCCACCACCTTGCCCTCCCAAGTCTGGATTACAGT 452
Qy 2112 GTGAGCCAC 2120
Db 451 GTGAGCCAC 443

RESULT 41
A0542542 596 bp DNA linear GSS 19-MAY-1999
LOCUS A0542542
DEFINITION RPECI-11-347J18.TV RPECI-11 Homo sapiens genomic clone RPECI-11-347J18
DNA sequence.
ACCESSION A0542542
VERSION A0542542.1 GI:4872998
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 596)
ZHAO, S., ADAMS, M.D., NIEMAN, W., MALEK, J., DE JONG, P. and VENTER
J.C.
Use of BAC End Sequences from Library RPECI-11 for Sequence-Ready
Map Building
Unpublished (1997)
JOURNAL Other GSSs: RPECI-11-347J18.TV
COMMENT Contact: Shaying Zhao, William Nieman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeet@igir.org
Clones are derived from the human BAC library RPECI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@jongs.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering/) or from
Research Genet Co (info@resgen.com). BAC end search page:
http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: 17
Class: BAC ends.

FEATURES
source
1..596
/organism="Homo sapiens"
/db_xref="GDB:7633097"
/db_xref="taxon:9606"
/clone_id="RPECI-11-347J18"
/clone_1id="RPECI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RC111 Human Male BAC Library"
BASE COUNT 145 a 143 c 109 g 198 t 1 others
ORIGIN

Query Match 2.7%; Score 69; DB 17; Length 596;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2052 GAATCTCTGACCTGAGGTGATCCACCACCTTGCCCTCCCAAGTCTGGATTACAGT 2111
Db 503 GAATCTCTGACCTGAGGTGATCCACCACCTTGCCCTCCCAAGTCTGGATTACAGT 562
Qy 2112 GTGAGCCAC 2120
Db 563 GTGAGCCAC 571

RESULT 42
A0348722/c

LOCUS AQ348722 617 bp DNA linear GSS 07-MAY-1999
 DEFINITION RPII11-11617.TJ RPII-11 Homo sapiens genomic clone RPII-11-11617,
 DNA sequence.
 ACCESSION AQ348722
 VERSION AQ348722.1 GI:4173618
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 617)
 AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
 J.C.
 TITLE Use of BAC End Sequences from Library RPII-11 for Sequence-Ready
 Map Building
 JOURNAL Unpublished (1997)
 COMMENT Other_GSSs: RPII11-11617.TV
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org
 Clones are derived from the human BAC library RPII-11. For BAC
 library availability, please contact Pieter de Jong
 (peter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from
 Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tcdb/hungen/bac_end_search/bac_end_search.html
 Seq primer: SP6
 Class: BAC ends.
 FEATURES
 source location/Qualifiers
 1..617
 /organism="Homo sapiens"
 /db_xref="GDB:754358"
 /db_xref="taxon:9606"
 /clone="RPII-11-11617"
 /clone_id="RPII-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPII11 Human Male BAC Library"
 BASE COUNT 143 a 140 c 142 g 192 t
 ORIGIN
 Query Match 2.7%; Score 69; DB 17; Length 617;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2052 GAATCTGACCTGACGATGATCCACCACTTGCGCTCCCAAGTGTGGATTAAGGT 2111
 Db 291 GAATCTGACCTGACGATGATCCACCACTTGCGCTCCCAAGTGTGGATTAAGGT 232
 Oy 2112 GTGAGCCAC 2120
 Db 231 GTGAGCCAC 223
 RESULT 43
 A1902426/c 262 bp mRNA linear EST 30-MAR-2000
 LOCUS A1902426
 DEFINITION CM-BT006-080299-139 BT006 Homo sapiens cDNA, mRNA sequence.
 ACCESSION A1902426
 VERSION A1902426.1 GI:649813
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 262)
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
 Brunstein,A., deoliveira,P.S., Bucher,P., Jorgensen,C.V., O'Hare
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/seq/gethtml.pl?tl=CM&t2=CM-BT006-139.html>)
 Seq primer: pUC 18 forward.
 FEATURES
 source location/Qualifiers
 1..262
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="BT006"
 /dev_stage="Adult"
 /sex="Female"
 /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
 SmaI; A mini-library was made by cloning products derived
 from ORFESTS PCR (U.S. Letters Patent application No. 196
 ,716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."
 BASE COUNT 83 a 58 c 68 g 44 t 9 others
 ORIGIN
 Query Match 2.6%; Score 68; DB 9; Length 262;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2053 AACTCTGACCTGACGATGATCCACCACTTGCGCTCCCAAGTGTGGATTAAGGT 2112
 Db 193 AACTCTGACCTGACGATGATCCACCACTTGCGCTCCCAAGTGTGGATTAAGGT 134
 Oy 2113 TGAGCCAC 2120
 Db 133 TGAGCCAC 126
 RESULT 44
 BF753734/c 420 bp mRNA linear EST 10-JAN-2001
 LOCUS BF753734
 DEFINITION IL5-CT0521-031000-163-f02 CT0521 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF753734
 VERSION BF753734.1 GI:12080410
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 420)
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
 Brunstein,A., deoliveira,P.S., Bucher,P., Jorgensen,C.V., O'Hare
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP
Brazil

FEATURES	Location/Qualifiers
source	1. .420

BASE COUNT	127 a	86 c	113 g	94 t
ORIGIN				

Query Match 2.6%; Score 68; DB 12; Length 420;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 45	LOCUS	DEFINITION	ACCSSION	VERSION	KEYWORDS	SOURCE
AO583583	AO583583	436 bp DNA linear	AO583583	AO583583	GS	human.
		RPCT-11-454D13.TV RPCT-11 Homo sapiens genomic clone RPCT-11-454D13		AO583583.1	GI:5010693	

REFERENCE AUTHORS	TITLE	JOURNAL COMMENT
1. (baees 1 to 436) Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter J.C.	Use of BAC End Sequences from Library RPc1-11 for Sequence-Ready Map Building	Unpublished (1997) Ocher_GSSs: RPc1-11-45HD13.TU Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel.: 301.838.0200 Fax: 301.838.0208 Email: hbe@igr.org
	Clones are derived from the human BAC library RPc1-11. For BAC library availability, please contact Pieter de Jong (piederdejong.med.bu@ro.ato.edu). Clones may be purchased from BAC/CPC Resources (http://bacpac.med.bu@ro.ato.edu/ordering) or from	

FEATURES

Source	1. .436
Location/Qualifiers	
Class: BAC ends.	
Seq Primer: 17	
Research Genet cs (info@sgen.com) . BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html	

```

/organism="Homo sapiens"
/db_xref="GDB:7674035"
/db_xref="taxon:9606"
/clone="RPCT-11-454D13"
/clone_1td="RPCT-11"
/sex="Male"
/cell_type="Lymphocytes"
/ncbi_vector="pBACe3.6; Site 1: EcoRI; Site 2: EcoRI
RPCT11 Human Male BAC Library"
BASE COUNT      75 a      148 c      91 g      121 t      1 others
ORIGIN

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Query Match	2.8%	Score 68	DB 17	Length 436
Best Local Similarity	100.0%	Pred. No. 0		
Matches	68	Conservative	0	Mismatches 0
				Indels 0
				Gaps 0
Qy	2053	AACTCTGACCTCAGATGATCCACCCACTTGAGCGCTCCCAAAGTGTGGGATTACAGGTG	2112	
Db	83	AACTCTGACCTCAGATGATCCACCCACTTGAGCGCTCCCAAAGTGTGGGATTACAGGTG	142	
Qy	2113	TGAGCGAC	2120	
Db	143	TGAGCGAC	150	

RESULT	46
LOCUS	A0462891
DEFINITION	A0462891 531 bp DNA linear GSS 23-APR-1996
ACCESSION	HS-5512.A1-B12 77A RCCT-11 Human Male BAC Library Homo sapiens genomic clone Plate=188 Col=23 Row=C, DNA sequence.
VERSION	A0462891
KEYWORDS	A0462891.1 GI:4635661 GSS.
SOURCE	human.
ORGANISM	human sapiens
REFERENCE	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 531)
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE	99380589
COMMENT	Contact: Mahairas GG, wallace JC, Hood L

```
FEATURES      Location/Qualifiers
      source      1..531
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="Plate=788 Col=23 Row=C"
```

ORIGIN
Query Match 2.6%; Score 68; DB 17; Length 531;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/clone_lib="RPCT-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBAC3.6 vector at EcoRI sites"

BASE COUNT 148 a 123 c 101 g 146 t 13 others

Query Match 2.6%; Score 68; DB 17; Length 531;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/clone_lib="RPCT-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBAC3.6 vector at EcoRI sites"

QY 2053 AACTCTGACCTGAGTGATCCACCCAGCTGCTCCCAAGTGGATTCAGAGTG 2112
DB 432 AACTCTGACCTGAGTGATCCACCCAGCTGCTCCCAAGTGGATTCAGAGTG 491

QY 2113 TGAGCCAC 2120
DB 492 TGAGCCAC 499

RESULT 47
LOCUS A0556467 546 bp DNA linear GSS 29-MAY-1999
DEFINITION HS_5236_B1.C01.T7A.RPCT-11 Human Male BAC Library Homo sapiens
ACCESSION A0556467
VERSION A0556467.1 GI:4916199
KEYWORDS GSS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 546)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, D., Zhao, S., Adams, M.D. and
Hood, L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCT-11. For BAC
library availability, please contact Pieter de Jong
pieterdejong.med.buffalo.edu. Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering/bac.htm)
or from Research Genetics (info@resgen.com). BAC end Web Server:
http://www.hsc.washington.edu
plate: 812 row: F column: 1
Seq primer: 17
Class: BAC ends
High quality sequence stop: 546.
Location/Qualifiers
1..546
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate:812 Col=1 Row=F"
/clone_lib="RPCT-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBAC3.6 vector at EcoRI sites"

BASE COUNT 135 a 120 c 173 g 108 t 10 others

ORIGIN
Query Match 2.6%; Score 68; DB 17; Length 546;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ATTTCCTGATGATGCTGCTGAGTGCTGCTGCTGAGGACATGGAGATTCGCCAG 431
DB 383 ATTTCCTGATGATGCTGCTGAGTGCTGCTGCTGAGGACATGGAGATTCGCCAG 442

QY 432 CAGAGAA 439
DB 443 CAGAGAA 450

RESULT 48
LOCUS AG14939/c 701 bp DNA linear GSS 08-JAN-2002
DEFINITION Pan troglodytes DNA, clone: RP43-006B10.T7, genomic survey
sequence.
ACCESSION AG14939
VERSION AG14939.1 GI:16674617
KEYWORDS GSS
SOURCE Pan troglodytes male lymphocytes DNA, clone RPCT-43 Chimpanzee
Male BAC Library clone: RP43-006B10.T7.
ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Torok, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of library RPCT-43
2 (bases 1 to 701)
Unpublished
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Torok, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Aaso Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9111, Fax: 81-45-503-9170
E-mail: chimpanzee@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/
Clones are derived from the chimpanzee BAC library RPCT-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector : pBAC3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1..701
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-006B10.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCT-43 Chimpanzee Male BAC Library"

COMMENT
LIBRARY
Vector : pBAC3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1..701
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-006B10.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCT-43 Chimpanzee Male BAC Library"

BASE COUNT 212 a 145 c 159 g 185 t
ORIGIN
Query Match 2.6%; Score 68; DB 17; Length 701;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AACTCTGACCTGAGTGATCCACCCAGCTGCTCCCAAGTGGATTCAGAGTG 2112
DB 194 AACTCTGACCTGAGTGATCCACCCAGCTGCTCCCAAGTGGATTCAGAGTG 135

QY 2053 AACTCTGACCTGAGTGATCCACCCAGCTGCTCCCAAGTGGATTCAGAGTG 2112
DB 194 AACTCTGACCTGAGTGATCCACCCAGCTGCTCCCAAGTGGATTCAGAGTG 135

QY 2113 TGAGCCAC 2120
DB 134 TGAGCCAC 127

BASE COUNT 135 a 120 c 173 g 108 t 10 others

RESULT 49
 BG718999/c 742 bp mRNA linear EST 08-MAY-2001
 LOCUS 602699111F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4831083 5',
 DEFINITION mRNA sequence.
 ACCESSION BG718999
 VERSION BG718999.1 GI:13398186
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 742)
 NIH-MGC http://mgs.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cga@gsf-rmmail.nih.gov
 Tissue Procurement: Miklos Palakovic, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shireki
 Tohiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLN at:
 http://image.lnl.gov
 Plate: L1AM10753 row: e column: 04
 High quality sequence stop: 740.
 Location/Qualifiers
 source 1..742
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="NIH_MGC_97"
 /db_host="DHI0B"
 /note="Organ: testis; Vector: pBluescript (modified
 pBluescript KS+); Site 1: BamHI, Site 2: SalI-XhoI (GCGAG
); Oligo-dT primed using primer 5'-TTTTTTTTTTT-3',
 size-selected for average insert size 2.2 kb and
 normalized to 10^5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NHGRI/NIH), National
 Institutes of Health. Note: this is a NIH_MGC Library."
 BASE COUNT 232 a 167 c 144 g 199 t
 ORIGIN
 Query Match 2.6%; Score 66; DB 12; Length 742;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2055 CTCCTGACCTCAGGTGATCCACCCACTTGGCTCCCAAGTCTGGATTACAGTGTG 2114
 Db 671 CTCCTGACCTCAGGTGATCCACCCACTTGGCTCCCAAGTCTGGATTACAGTGTG 612
 Oy 2115 AGCCAC 2120
 Db 611 AGCCAC 606
 RESULT 50
 AQ675390/c 472 bp DNA linear GSS 24-JUN-1999
 LOCUS HS_2151_A1_D03_T7C_CIT Approved Human Genomic Sperm Library D Homo
 DEFINITION sapiens genomic clone Plate=2151 Col=5 Row=G, DNA sequence.
 ACCESSION AQ675390
 VERSION AQ675390.1 GI:5208136
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 472)
 AUTHORS Mahairas G.G., Wallace J.C., Smith K., Swartzell S., Holman T.,
 Keller A., Shaker R., Furlong J., Young J., Zhao S., Adams M.D. and
 Hood L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@regen.com).
 BAC end Web Server: http://www.htsc.washington.edu
 Plate: 2151 row: G column: 5
 Seq primer: 17
 Class: BAC ends
 High quality sequence stop: 472.
 Location/Qualifiers
 source 1..472
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="Plate=2151 Col=5 Row=G"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /sex="male"
 /note="Organ: sperm; Vector: pBel0BAC11; BAC clones in
 E-Coli DH10B"
 BASE COUNT 143 a 73 c 95 g 158 t 3 others
 ORIGIN
 Query Match 2.5%; Score 65; DB 17; Length 472;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2056 TCCCTACCTCAGGTGATCCACCCACTTGGCTCCCAAGTCTGGATTACAGTGTGA 2115
 Db 356 TCCCTACCTCAGGTGATCCACCCACTTGGCTCCCAAGTCTGGATTACAGTGTGA 297
 Oy 2116 GCCAC 2120
 Db 296 GCCAC 292
 RESULT 51
 AU145455 579 bp mRNA linear EST 05-AUG-2002
 LOCUS AU145455 HEMBA1 Homo sapiens cDNA clone HEMBA1004880 3', mRNA
 DEFINITION sequence.
 ACCESSION AU145455
 VERSION AU145455.1 GI:11006976
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 579)
 Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
 Yamamoto, J., Wakamatsu, A., Ozawa, M., Nakamura, Y., Nagai, T., Sugano
 S. and Iwagaki, T.).
 HRI human cDNA project (Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S.,
 Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Ozawa, M., Nakamura
 Y., Nagai, T., Sugano, S., Iwagaki, T.)
 TITLE HRI human cDNA project (Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S.,
 Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Ozawa, M., Nakamura
 Y., Nagai, T., Sugano, S., Iwagaki, T.)
 JOURNAL Unpublished (2000)
 COMMENT Contact: Takao Iwagaki
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986

Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
 Research Institute; cDNA library construction: Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.

FEATURES

Source

1. 579
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="HEMBA1004880"
 /clone_id="HEMBA1"
 /tissue_type="whole embryo, mainly head"
 /dev_stage="embryo, 10 weeks"
 /note="Vector: PM18SFL3"

BASE COUNT 146 a 133 c 111 g 181 t 8 others

ORIGIN

Query Match 2.5%; Score 65; DB 9; Length 579;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2056 TCCGACCTCAGGTATCCACCCACCTTGCCTCCCAAGCTGGGATTACAGGTGGA 2115
 Db 329 TCCGACCTCAGGTATCCACCCACCTTGCCTCCCAAGCTGGGATTACAGGTGGA 388

Qy 2116 GCCAC 2120
 Db 389 GCCAC 393

RESULT 52

LOCUS

N22395 448 bp mRNA linear EST 20-DEC-1995
 YW37108.s1 Morton Fetal Cochlea Homo sapiens cDNA clone

DEFINITION

IMAGE:254439.3, similar to contains Alu repetitive element; mRNA
 sequence.

ACCESSION

N22395
 N22395.1 GI:1128529

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 448)
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B.,
 Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins,
 M., Hiltman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
 B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
 Schenkelberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
 Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Wirtz, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)

TITLE

JOURNAL

MEDLINE

COMMENT

Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 High quality sequence stops: 346
 Source: IMAGE Consortium, LML
 This clone is available royalty-free through LML; contact the
 IMAGE Consortium (info@image.lml.gov) for further information.
 Insert Length: 844 Std Error: 0.00
 Seq primer: m13 -40 forward
 High quality sequence stop: 346.

FEATURES

Source

1. 448
 /organism="Homo sapiens"
 /db_xref="GDB:3891892"
 /db_xref="taxon:9606"
 /clone="IMAGE:254439"
 /clone_id="Morton Fetal Cochlea"

/tissue_type="cochlea"
 /dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /note="Organ: ear; Vector: pBluescript SK-; Site 1: EcoRI;
 Site 2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
 unidirectionally. Primer: Oligo dt. Fetal cochlea, normal.
 37 of inserts < 0.5 kb, 56% 0.5-1.0 kb, 7% > 1 kb. Uni-ZAP
 XR Vector. Library constructed by N. Robertson, C. Morton.
 -5' adaptor sequence: 5' GAATTCGACGAG 3' -3' adaptor
 sequence: 5' CTCGAGTTTATTTTATTTT 3"

BASE COUNT 124 a 105 c 94 g 122 t 3 others

ORIGIN

Query Match 2.5%; Score 63; DB 14; Length 448;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2058 CTGACCTCAGGTATCCACCCACCTTGCCTCCCAAGCTGGGATTACAGGTGAGC 2117
 Db 214 CTGACCTCAGGTATCCACCCACCTTGCCTCCCAAGCTGGGATTACAGGTGAGC 273

Qy 2118 CAC 2120
 Db 274 CAC 276

RESULT 53

LOCUS

A0531017 457 bp DNA linear GSS 18-MAY-1999
 RPCT-11-373D14.TV RPCT-11 Homo sapiens genomic clone RPCT-11-373D14
 DNA sequence.

DEFINITION

A0531017 457 bp DNA linear GSS 18-MAY-1999
 RPCT-11-373D14.TV RPCT-11 Homo sapiens genomic clone RPCT-11-373D14
 DNA sequence.

ACCESSION

A0531017
 A0531017.1 GI:4843060

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Use of BAC End Sequences from Library RPCT-11 for Sequence-Ready
 Map Building
 Unpublished (1997)
 Other GSSs: RPCT-11-373D14.TV
 Contact: Shaying Zhao, William Niernan, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@igr.org
 Clones are derived from the human BAC library RPCT-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genet. Co. (http://resgen.com). BAC end search page:
 http://www.igr.org/cdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: T7
 Clases: BAC ends.

FEATURES

Source

1. 457
 /organism="Homo sapiens"
 /db_xref="GDB:7642933"
 /db_xref="taxon:9606"
 /clone="RPCT-11-373D14"
 /clone_id="RPCT-11"
 /sex="Male"
 /cell_type="Tymphocytoid"
 /note="Vector: pBAC3.6; Site 1: EcoRI, Site 2: EcoRI;
 RPCT11 Human Male BAC Library"

BASE COUNT

127 a 79 c 115 g 136 t

Query Match 2.5%; Score 63; DB 17; Length 457;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2058 CTGACCTGAGTATCCACCCACCTTGCGCTCCCAAGTCTGGGATTACAGTGTAGC 2117

DB 286 CTGACCTGAGTATCCACCCACCTTGCGCTCCCAAGTCTGGGATTACAGTGTAGC 227

OY 2118 CAC 2120

DB 226 CAC 224

RESULT 54
A0635302
LOCUS
DEFINITION RPT-11-475A11.TV RPT-11 Homo sapiens genomic clone RPT-11-475A11

621 bp DNA linear GSS 17-JUN-1999
A0635302
VERSION A0635302.1 GI:5097937

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 621)

AUTHORS Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.

TITLE Use of BAC End Sequences from Library RPT-11 for Sequence-Ready

JOURNAL Map Building
Unpublished (1997)

COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0208

Email: hbeet@igf.org

Clones are derived from the human BAC library RPT-11. For BAC

library availability, please contact Pieter de Jong

(pieter@igf.org, med.bufileo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.bufileo.edu/ordering) or from

Research Genet cs (info@resgen.com). BAC end search page:

http://www.igf.org/cdb/humgen/bac_end_search/bac_end_search.html.

Seq primer: 17

Class: BAC ends.

Location/Qualifiers

1..621

/organism="Homo sapiens"

/db_xref="GDB:768202.6"

/db_xref="taxon:9606"

/clone="RPT-11-475A11"

/clone_11b="RPT-11"

/sex="Male"

/cell_type="Lymphocytes"

/note="Vector: PAC3.6; Site_1: EcoRI; Site_2: EcoRI;

RPT-11 Human Male BAC Library"

RESULT 55

A0859931

LOCUS

DEFINITION QV1-CT0364-260100-052-g03 CT0364 Homo sapiens cDNA, mRNA sequence.

ACCESSION A0859931

VERSION A0859931.1 GI:795624

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 433)

AUTHORS Dias Neto, E., Garcia Correa, R., Vertovskii, Almeida, S., Brites, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsushima, A., Bala, G.S., Simpson, D.H.,

Brustein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,

M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.V. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

2020263

CONTACT: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/bcr/pts/gethtml2.pl?l=ct2=QV1-CT0364-260

100-052-g03&ct3=2000-01-26&ct4=1)

Seq primer: puc 18 forward

High quality sequence start: 49

High quality sequence stop: 433.

Location/Qualifiers

1..433

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_11b="CT0364"

/dev_stage="Adult"

/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:

SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No. 196

,716 - Ludwig Institute for Cancer Research) profiles

into the pUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

BASE COUNT 121 a 111 c 108 g 93 t

ORIGIN

Query Match 2.4%; Score 62; DB 10; Length 433;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2059 TGACCTGAGTATCCACCCACCTTGCGCTCCCAAGTCTGGGATTACAGTGTAGC 2118

DB 171 TGACCTGAGTATCCACCCACCTTGCGCTCCCAAGTCTGGGATTACAGTGTAGC 112

OY 2119 AC 2120

DB 111 AC 110

RESULT 56

A0343967

LOCUS

DEFINITION RPT-11-112J16.TU RPT-11 Homo sapiens genomic clone RPT-11-112J16,

DNA sequence.

ACCESSION A0343967

543 bp DNA linear GSS 07-MAY-1999

VERSION A043967.1 GI:4168863
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 543)
 AUTHORS Zhao, S., Adams, M.D., Nieman, W., Malek, J., de Jong, P. and Venter
 J.C.
 TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
 Map Building
 JOURNAL Unpublished (1997)
 COMMENT Other GSSs: RPCI11-112016.TV
 Contact: Shaying Zhao, William Nieman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@jlong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genetics (info@resgen.com). BAC end search page:
 http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html
 Seq primer: SP6
 Class: BAC ends.
 FEATURES
 source
 Location/Qualifiers
 1..543
 /organism="Homo sapiens"
 /db_xref="GDB:7542855"
 /db_xref="taxon:9606"
 /clone_lib="RPCI-11-112016"
 /clone_id="RPCI-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPCI11 Human Male BAC library"
 BASE COUNT 127 a 138 c 131 g 147 t
 ORIGIN
 Query Match 2.4%; Score 62; DB 17; Length 543;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2059 TGACCTGAGTATCCACCACTTGCGCTCCAAAGTGGATTACAGGTGAGCC 2118
 |||||||
 DB 359 TGACCTGAGTATCCACCACTTGCGCTCCAAAGTGGATTACAGGTGAGCC 418
 QY 2119 AC 2120
 ||
 DB 419 AC 420
 RESULT 57
 A0435006/c 593 bp DNA linear GSS 31-MAR-1999
 LOCUS HS-5114_B2_A08 T7A RPCI-11 Human Male BAC Library Homo sapiens
 DEFINITION genomic Clone Plate=690 Col=16 Row=B, DNA sequence.
 ACCESSION A0435006
 VERSION A0435006.1 GI:4546345
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 593)
 AUTHORS Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
 Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
 Hood, L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@jlong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
 or from Resear h Genetics (info@resgen.com). BAC end Web Server:
 http://www.htsc.washington.edu
 plate: 690 row: B column: 16
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 593.
 FEATURES
 source
 Location/Qualifiers
 1..593
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Plate=690 Col=16 Row=B"
 /clone_id="RPCI-11 Human Male BAC library"
 /sex="male"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBAC3.6 vector at EcoRI sites"
 BASE COUNT 150 a 158 c 117 g 142 t 26 others
 ORIGIN
 Query Match 2.4%; Score 62; DB 17; Length 593;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2059 TGACCTGAGTATCCACCACTTGCGCTCCAAAGTGGATTACAGGTGAGCC 2118
 |||||||
 DB 337 TGACCTGAGTATCCACCACTTGCGCTCCAAAGTGGATTACAGGTGAGCC 278
 QY 2119 AC 2120
 ||
 DB 277 AC 276
 RESULT 5B
 AM470105 174 bp mRNA linear EST 24-FEB-2000
 LOCUS X72912.X1 NCI CGAP UT4 Homo sapiens cDNA clone IMAGE:2761606 3'
 DEFINITION similar to contains Alu repetitive element; contains element MER35
 ACCESSION AM470105
 VERSION AM470105.1 GI:7040211
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 174)
 NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be

```
/tissue_type="germinal center B cell"  
/lab_host="DH10B"
```

polylinker: Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20⁺, IgD⁺), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo (dT) primer
(5'-TCCTTACCAATCTCATAGTGGAGCGCCGCCCTCTTTTCTTTTCTTTT-3'). Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization and was constructed by Bento Soares and M. Fatima Bonaldo."

2.44; Score 61; DB 9; Length 214;
Identity 100.0%; Pred. No. 0;
Insertions 0; Mismatches 0; Indels 0; Gaps 0;
a 62 c 52 g 58 t

GRACCTCAGGTATTCACCCACCTTGCCCTCCCAAGTGTCTGGATTTCAG 2109
GACCTCAGGTATTCACCCACCTTGCCCTCCCAAGTGTCTGGATTTCAG 207

224 bp mRNA linear EST 14-JUN-2001
86-610201-837-d01 MT0286 Homo sapiens cDNA, mRNA sequence.
.1 GI:14431627

10.0.5.1 to 234
a; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
a; Euteleostomi; Primates; Catarrhini; Homnidae; Homo.
O.E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
G.H., Garvalho, A.F., Matsumura, A., Bata, G.S., Simpson, D.H.,
n.A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
Coates, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
A.J.

sequencing of the human transcriptome with ORF expressed
tags
Cl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

Simpson A.J.G.
Institute for Cancer Genetics
Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
-11-2704922
-11-2707001
simspon@ludwig.org.br
This entry can be seen in the following URL
www.ludwig.org.br/scripts/gethtml2.pl?rl=CM4&t=CM4-MT0286-1
37-d01&t3=2001-02-01&t4=1)
er: puc 18 forward
lity sequence start: 29
lity sequence stop: 214.
Location/Qualifiers
1..234
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MT0286"
/dev_stage="Adult"
note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived

RESULT 63
AA93165 346 bp mRNA linear EST 27-AUG-1998
LOCUS
DEFINITION
AA93165.1 Soares total fetus Nb2H8.9w Homo sapiens cDNA clone
IMAGE:1622800.3' similar to contains Alu repetitive element, mRNA
sequence.

ACCESSION
AA93165
VERSION
AA93165.1 GI:3179710
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 346)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LIND; contact the
IMAGE Consortium (info@image.lind.gov) for further information.
Insert Length: 1727 Std Error: 0.00
Seq primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 338.

FEATURES
source
1. 346
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1622800"
/clone_1lb="Soares total_fetus_Nb2H8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTTACCACTCGAAGCGAGCGCGCTCAATTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT
78 a 94 c 75 g 99 t

ORIGIN
Query Match 2.4%; Score 61; DB 9; Length 346;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2050 TCGAATCTCTGACCTGAGTGATCCACCCACCTTGGCTCCCAAGTCTGGATTACG 2109
Db 204 TCGAATCTCTGACCTGAGTGATCCACCCACCTTGGCTCCCAAGTCTGGATTACG 263

QY 2110 G 2110
Db 264 G 264

RESULT 64
AV762430 350 bp mRNA linear EST 19-OCT-2000
LOCUS
DEFINITION
AV762430.1 Homo sapiens cDNA clone MDSBDF09.5', mRNA sequence.
ACCESSION
AV762430
VERSION
AV762430.1 GI:10920278
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 350)
Gu, Y., Zhao, M., Huang, Q., Xu, X., Li, Y., Peng, Y., Song, H., Xiao, H.,
Gu, Y., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng

TITLE
JOURNAL
COMMENT
L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G.,
Yang, Y., Gao, G., Zhang, Q., Chen, S., Han, Z., and Chen, Z.
Homo sapiens cDNA MDS clones
Unpublished (2000)
Contact: Zenguan Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1. 350
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MDSBDF09"
/clone_1lb="MDS"
/issue_type="Bone marrow"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/note="Vector: pT73D-Pac; Site_1: SfiI; Site_2: SfiI"

BASE COUNT
93 a 86 c 100 g 71 t

ORIGIN
Query Match 2.4%; Score 61; DB 10; Length 350;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2050 TCGAATCTCTGACCTGAGTGATCCACCCACCTTGGCTCCCAAGTCTGGATTACG 2109
Db 80 TCGAATCTCTGACCTGAGTGATCCACCCACCTTGGCTCCCAAGTCTGGATTACG 21

QY 2110 G 2110
Db 20 G 20

RESULT 65
AA731898 377 bp mRNA linear EST 07-FEB-1998
LOCUS
DEFINITION
AA731898.1 NCI-CCAP GCBI Homo sapiens cDNA clone IMAGE:1252051.3'
similar to contains Alu repetitive element; contains element PTR5
repetitive element; mRNA sequence.

ACCESSION
AA731898
VERSION
AA731898.1 GI:2752709
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 377)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIND at:
www-bio.lind.gov/bdip/image/image.html
Insert Length: 1654 Std Error: 0.00
Seq primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 376.

FEATURES
source
1. 377
/organism="Homo sapiens"

TITLE /I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
Unpublished (2000)

JOURNAL Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: john@tigr.org
Plate: 286

COMMENT Seq primer: Forward.
Location/Qualifiers
1..501
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequencing, MAGE"
/note="Vector: pBluescriptKS"

BASE COUNT 119 a 128 c 150 g 104 t
ORIGIN

Query Match 2.4%; Score 61; DB 10; Length 501;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2050 TCGAAGCTGAGCTGATCCACCCAGCTTGGCTCCCAAGTCTGGATTACAG 2109
Db 188 TCGAAGCTGAGCTGATCCACCCAGCTTGGCTCCCAAGTCTGGATTACAG 129

Qy 2110 G 2110
Db 128 G 128

RESULT 73
LOCUS AW753552 568 bp mRNA linear EST 28-APR-2000
DEFINITION PM3-CT0264-151099-001-G05 CT0264 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW753552
VERSION AW753552.1 GI:7668484
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 568)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldmann, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

FEATURES
source 1..568
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0264"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ONESTES PCR (U.S. Letters Patent Application No. 196 /16 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 140 a 118 c 112 g 198 t
ORIGIN

Query Match 2.4%; Score 61; DB 10; Length 568;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2050 TCGAAGCTGAGCTGATCCACCCAGCTTGGCTCCCAAGTCTGGATTACAG 2109
Db 164 TCGAAGCTGAGCTGATCCACCCAGCTTGGCTCCCAAGTCTGGATTACAG 223

Qy 2110 G 2110
Db 224 G 224

RESULT 74
LOCUS AM806847 613 bp mRNA linear EST 17-MAY-2000
DEFINITION MR0-ST0020-201099-003-b12 ST0020 Homo sapiens cDNA, mRNA sequence.
ACCESSION AM806847
VERSION AM806847.1 GI:7899841
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 613)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldmann, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

FEATURES
source 1..613
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0020"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ONESTES PCR (U.S. Letters Patent Application No. 196 /16 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 140 a 118 c 112 g 198 t
ORIGIN

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High quality sequence stop: 594.
Location/Qualifiers
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/note="Organ: stomach; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ONESTES PCR (U.S. Letters Patent Application No. 196 /16 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

Search completed: March 30, 2003, 19:49:22
 Job time : 4114 secs

derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 142 a 149 c 193 g 129 t
 ORIGIN

Query Match 2.4%; Score 61; DB 10; Length 613;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2052 GAACCTCCTGACCTGAGTATCCACCCAGCTTGGCTCCCAAGTGTGGATTACAGT 2111
 DB 433 GAACCTCCTGACCTGAGTATCCACCCAGCTTGGCTCCCAAGTGTGGATTACAGT 374

QY 2112 G 2112
 DB 373 G 373

RESULT 75
 AV733872/c 618 bp mRNA linear EST 17-OCT-2000

LOCUS AV733872 cda Homo sapiens cDNA clone cdaSG06 5', mRNA sequence.

DEFINITION AV733872
 ACCESSION AV733872
 VERSION AV733872.1 GI:10851417

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 618)
 Yang, Y., Song, H., Peng, Y., Gu, Y., Gao, G., Xiao, H., Xu, X., Li, N.,

Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu
 W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J.,

Chen, Z. and Han, Z.
 Homo sapiens cDNA clones

Unpublished (2000)

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351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China

Tel: 86-21-50801919 (ex.45)
 Fax: 86-21-50801922

Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES
 Location/Qualifiers

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/clone_id="cdaSG06"

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/dev_stage="Adult"

/lab_host="BM25.8"

/note="vector: pT7-1ex2; Site_1: sf1A; Site_2: sf1B"

BASE COUNT 136 a 203 c 142 g 135 t 2 others

ORIGIN

Query Match 2.4%; Score 61; DB 10; Length 618;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2050 TCGAATCTGACCTGAGTATCCACCCAGCTTGGCTCCCAAGTGTGGATTACAG 2109
 DB 563 TCGAATCTGACCTGAGTATCCACCCAGCTTGGCTCCCAAGTGTGGATTACAG 504

QY 2110 G 2110
 DB 603 G 503